

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 3, 2006, 19:32:24 ; Search time 212 Seconds  
 (without alignments)  
 2847.672 Million cell updates/sec

Title: US-10-079-185-2

Perfect score: 7500  
 Sequence: 1 MMQGNTCHRMSPHPGRGPR.....MRWEREHOEREPDETEDKK 1374

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439376781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : A\_Geneseq\_21:\*

1: geneseqP1990B:\*

2: geneseqP1990B:\*

3: geneseqP2001B:\*

4: geneseqP2001B:\*

5: geneseqP2002B:\*

6: geneseqP2003As:\*

7: geneseqP2003Bs:\*

8: geneseqP2004B:\*

9: geneseqP2005B:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Length	DB ID	Description	ALIGNMENTS
1	7500	100.0	1374	8 ADDQ96675	RESULT 1 ADDQ96675
2	7500	100.0	1374	8 ADD68727	ID ADDQ96675 standard; protein; 1374 AA.
3	7500	100.0	1374	9 AEB47411	XX
4	7486	99.8	1374	8 ADD17464	XX
5	7486	99.8	1374	9 ADD17386	XX
6	7483.5	99.8	1373	7 ABU63361	XX
7	6426	85.7	1200	9 AEB20195	XX
8	6062	80.8	1374	6 ABU08060	XX
9	4071	54.3	769	4 AAB92635	XX
10	2963	38.0	1327	4 ABB5839	XX
11	2847	38.0	541	6 ABM04841	XX
12	2519	33.6	486	9 AEB21037	XX
13	2463	32.6	466	8 ADD96710	XX
14	2463	32.6	8 ADD96710	XX	
15	1961	26.1	378	4 AAB21744	XX
16	1961	26.1	378	7 ADD46385	XX
17	1956	26.1	378	4 AAB20385	XX
18	1320	17.6	263	4 AAB21580	XX
19	1320	17.6	263	7 ADD46221	XX
20	1295.5	17.3	301	4 AAB63281	XX
21	1289	17.2	267	4 AAB63379	XX
22	1122	15.0	277	4 AAB63383	XX
23	890	11.9	412	8 ADD96676	XX
24	890	11.9	412	8 ADD96728	XX

PA	(CROO1) CROOKE S T.	Db	661 DWNLKGPFLFDSPPCCPFRHMPFRVFLPDGKEVLSMHOILYLLRCSKALVPEEIA 720
PA	(WUH1) WU H.	QY	721 NMLQBELEMOKYAECKGMVTINGTKEFSSVRIPDLDQFNPDPVITFPIVHGIRPA 780
XX		Db	721 NMLQBELEMOKYAECKGMVTINGTKEFSSVRIPDLDQFNPDPVITFPIVHGIRPA 780
PT	Crooke ST, Wu H;	QY	781 QLSYAGDPQOKUWKSIVKURHLLANSKQTKDQKLAQREALQKIRQNTMRETV 840
XX		Db	781 QLSYAGDPQOKUWKSIVKURHLLANSKQTKDQKLAQREALQKIRQNTMRETV 840
DR	WPI; 2004-516913/49.	QY	841 ELSOGCFWKURGIRSIVCQHAMMLPTLTHURYHOCMLMHLKLIGTFQDCLLQAMTHP 900
DR	N-PSDB; ADQ96674.	Db	841 ELSOGCFWKURGIRSIVCQHAMMLPTLTHURYHOCMLMHLKLIGTFQDCLLQAMTHP 900
XX		QY	841 ELSOGCFWKURGIRSIVCQHAMMLPTLTHURYHOCMLMHLKLIGTFQDCLLQAMTHP 900
PT	New isolated nucleic acid molecule encoding human RNase III, useful for research, biological or clinical purposes, e.g. defining the roles of RNase III and the interaction of human RNase III and cellular RNA.	Db	901 SHHLNFGMNPDHARISLNGCIRQPKYGRKVMHMKUGINTLNMRSRLIGQDPTPS 960
CC	invention is useful for research, biological and clinical purposes. It is useful in defining the roles of RNase III and the interaction of human RNase III and cellular RNA. The present sequence is the human RNase III enzyme.	QY	901 SHHLNFGMNPDHARISLNGCIRQPKYGRKVMHMKUGINTLNMRSRLIGQDPTPS 960
CC		Db	961 RINHNERLEFGDAVVELTSVHLVYLPSPLEGGIATYTAIVQHNLAMAKKELDP 1020
CC		Db	961 RINHNERLEFGDAVVELTSVHLVYLPSPLEGGIATYTAIVQHNLAMAKKELDP 1020
XX	Sequence 1374 AA;	QY	1021 FMLYANGPDDICRSDRURHAMANCERALIGAVYLESGSLEAKOLFRLFILENDPDLRERWLN 1080
SQ	Query Match 100.0%; Score 7500; DB 8; Length 1374; Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0; Matches 1374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Db	1021 FMLYANGPDDICRSDRURHAMANCERALIGAVYLESGSLEAKOLFRLFILENDPDLRERWLN 1080
QY	1 MNGQNTCHMRPHGRGCPGRGGHGRPSAQSFRPONTLHPPQOPPVQYQEPSSAPS 60	QY	1081 YPLHPLQJQBERTDROLIESTPVLQKLTERRAIGVIFPVTUMLRAFTTURVGENHTL 1140
Db	1 MNGQNTCHMRPHGRGCPGRGGHGRPSAQSFRPONTLHPPQOPPVQYQEPSSAPS 60	Db	1081 YPLHPLQJQBERTDROLIESTPVLQKLTERRAIGVIFPVTUMLRAFTTURVGENHTL 1140
QY	61 TTFNSNAPNPNPLPPDPFPVPPMPSAQGELPPCPIRPFPNQHMRHPPVPCFP 120	QY	1141 GHNORMELFLGSIMQVATEVLFIRPHDIGHFLMRSILVNRTOQAKVABLGQEA 1200
Db	61 TTFNSNAPNPNPLPPDPFPVPPMPSAQGELPPCPIRPFPNQHMRHPPVPCFP 120	Db	1141 GHNORMELFLGSIMQVATEVLFIRPHDIGHFLMRSILVNRTOQAKVABLGQEA 1200
QY	121 PFPMPCPNNPPVPGAPPGQGTPFPFMMPPSMHPPPPVMMQVNQYPPGSHINPPP 180	QY	1141 GHNORMELFLGSIMQVATEVLFIRPHDIGHFLMRSILVNRTOQAKVABLGQEA 1200
Db	121 PFPMPCPNNPPVPGAPPGQGTPFPFMMPPSMHPPPPVMMQVNQYPPGSHINPPP 180	Db	1141 GHNORMELFLGSIMQVATEVLFIRPHDIGHFLMRSILVNRTOQAKVABLGQEA 1200
QY	181 SFNSFQHNPSLPSANNSSSHFRHLLPPYLPKAPSERRSRSPRLKHYDDHHRDISHGR 240	QY	1201 ITNDKTKRPGVIRKTILADDLESFIALYTDQDLEVTHTFMVNCPPRKEFTILNDWD 1260
Db	181 SFNSFQHNPSLPSANNSSSHFRHLLPPYLPKAPSERRSRSPRLKHYDDHHRDISHGR 240	Db	1201 ITNDKTKRPGVIRKTILADDLESFIALYTDQDLEVTHTFMVNCPPRKEFTILNDWD 1260
QY	241 GERRHSLDRREFGRSPDRRROPSRYSRSDYDRRTPSRHSYRSRERERERHRDRNRS 300	QY	1261 PKSLOQOCCLTURTEKEPDLIPLKYLQTVGSHARTTYTAVYKGERIGCGKGSIQQA 1320
Db	241 GERRHSLDRREFGRSPDRRROPSRYSRSDYDRRTPSRHSYRSRERERERHRDRNRS 300	Db	1261 PKSLOQOCCLTURTEKEPDLIPLKYLQTVGSHARTTYTAVYKGERIGCGKGSIQQA 1320
QY	301 PSLSRSYKKEYRSGSAGYGLSVPEPAGCTPELPGETIKNTDSWAPLTIHRSPEK 360	QY	1321 EMGANDALEKYNPOMAHOKRPIKSKYRQBLKEMWREHQEREDDETDIKK 1374
Db	301 PSLSRSYKKEYRSGSAGYGLSVPEPAGCTPELPGETIKNTDSWAPLTIHRSPEK 360	Db	1321 EMGANDALEKYNPOMAHOKRPIKSKYRQBLKEMWREHQEREDDETDIKK 1374
QY	361 KWARWEERKDMDNGSSGKDKDNTSTKEKEPEETMDKNEEEEEEELKPKWIRCHSEN 420	RESULT 2	ADR68727
Db	361 KWARWEERKDMDNGSSGKDKDNTSTKEKEPEETMDKNEEEEEEELKPKWIRCHSEN 420	ID	ADR68727 standard; protein; 1374 AA.
QY	421 YVSSDPMDQVQGSDTUVGTSRILRDLYDKPEEEELGSROKAKARPWEPKTDLELESS 480	AC	ADR68727;
Db	421 YVSSDPMDQVQGSDTUVGTSRILRDLYDKPEEEELGSROKAKARPWEPKTDLELESS 480	XX	
QY	481 SFSECESEDEDSTCSSLSSDSEVVDIAEIKRKGAHPDLHDLWYWDQMGDQMGDICKCSA 540	DT	02-DEC-2004 (first entry)
Db	481 SFSECESEDEDSTCSSLSSDSEVVDIAEIKRKGAHPDLHDLWYWDQMGDQMGDICKCSA 540	XX	
QY	541 KARRTGTRHSTYFGEAEAKPCPMTNNAGRLHYRITVSPPTNFTDRPTVLEYDHEYI 600	DE	Human Ribonuclease III, RNase III.
Db	541 KARRTGTRHSTYFGEAEAKPCPMTNNAGRLHYRITVSPPTNFTDRPTVLEYDHEYI 600	XX	
QY	601 PEGFMSMFAHAPLTPNIPLCKVFRNIDYTHEFEMMPENFCVKGKLFSLFLFRDILEY 660	KW	Human; enzyme; Ribonuclease III; RNase III; RNA interference; Gene silencing; double stranded RNA; pre-rRNA processing; RNA processing; RNA expression; RNA splicing; RNA translocation.
Db	601 PEGFMSMFAHAPLTPNIPLCKVFRNIDYTHEFEMMPENFCVKGKLFSLFLFRDILEY 660	KX	
QY	661 DWNLKGFLFEDSPCPFRHMPFRVFLPDPGKEVLSMHQILYLLYURCSGALVPEEIA 720	OS	
PT		XX	Homo sapiens.
Db		Key	Location/Qualifiers
QY		Domain	1..220
Db		FT	/label = Proline rich domain
QY		FT	/note = "Claimed in claim 8"
Db		FT	221..470
QY		FT	/label = Serine Arginine rich domain
Db		FT	/note = "Claimed in claim 8"
QY		FT	949..174
Db		FT	/label = RNase III domain
QY		PT	/note = "Claimed in claim 8"



Db	1321 EMGAMDALEKVNFPQMAHQKRGFIGKRYQBLKEMRWEREHQEREPDTEDIKK 1374	SQ	Sequence 1374 AA;
RESULT	3	Query Match	100.0%; Score 7500; DB 9; Length 1374;
AEB47411	ID AEB47411 standard; protein; 1374 AA.	Best Local Similarity	100.0%; Pred. No. 0;
XX	AC AEB47411;	Matches	1374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX	DT 22-SEP-2005 (first entry)	QY	1 MMQGNTCHRMSPHGRGPRGRGGGARGARASAPSFRPONALHLRQOPPQVQYEPAPS 60
XX	DE Human ribonuclease III (RNase III) protein, SEQ ID NO: 2.	Db	1 MMQGNTCHRMSPHGRGPRGRGGGARGARASAPSFRPONALHLRQOPPQVQYEPAPS 60
XX	KW Ribonuclease; gene silencing; enzyme.	QY	61 TTFNSPAPNPLPPRDPFVPPPPMPSAGQPLPPCPTRIPFPNPHQMRHPFPVPPCFPPM 120
OS Homo sapiens.	XX	Db	61 TTFNSPAPNPLPPRDPFVPPPPMPSAGQPLPPCPTRIPFPNPHQMRHPFPVPPCFPPM 120
XX	FH Key	QY	121 PPPMCPNNPVPVGAPPGQSTPPFMMPSPSMPPMPPQMVQPCYSHNFP 180
FT Region	Region	FT	121 PPPMCPNNPVPVGAPPGQSTPPFMMPSPSMPPMPPQMVQPCYSHNFP 180
FT	/note= "RNase III serine-arginine rich region"	FT	121 PPPMCPNNPVPVGAPPGQSTPPFMMPSPSMPPMPPQMVQPCYSHNFP 180
FT	Domain	FT	121 PPPMCPNNPVPVGAPPGQSTPPFMMPSPSMPPMPPQMVQPCYSHNFP 180
FT	/note = RNase III domain	FT	121 PPPMCPNNPVPVGAPPGQSTPPFMMPSPSMPPMPPQMVQPCYSHNFP 180
FT	Misc-difference	FT	1211 /note= "Encoded by GCG"
FT	Region	FT	1262. .1269 /note= "Alpha helix"
FT	Region	FT	1282. .1290 /note= "Beta sheet"
FT	Region	FT	1297. .1303 /note= "Beta sheet"
FT	Region	FT	1308. .1315 /note= "Beta sheet"
FT	Region	FT	1318. .1336 /note= "Alpha helix"
FT	Misc-difference	FT	1345 /note= "Encoded by GAA"
XX	US2005159384-A1.	PN	181 SFNSFONNPPSFLPSANNSSPHFRFLPFLPKAPSERSPERJHYDHRHSHR 240
XX	PD 21-JUL-2005.	PD	181 SFNSFONNPPSFLPSANNSSPHFRFLPFLPKAPSERSPERJHYDHRHSHR 240
PP	02-DEC-2004; 2004US-00001993.	PR	241 GERMHSRDRBERGSPDRQDSRSRSDPGRGTRSRHRSYERSHRSYERERHRHNR 300
XX	06-JUL-2001; 2001US-00900425.	PR	241 GERMHSRDRBERGSPDRQDSRSRSDPGRGTRSRHRSYERSHRSYERERHRHNR 300
PR	20-FEB-2002; 2002US-00079185.	PR	361 KARARBEKEKORWSDNQSSGKDNYSIKEKEPEETMPKDRBEEBEEBLLKWMRICHSEN 420
XX	(ISIS-) ISIS PHARM INC.	PR	361 KARARBEKEKORWSDNQSSGKDNYSIKEKEPEETMPKDRBEEBEEBLLKWMRICHSEN 420
XX	PI Crooke ST;	PR	361 KARARBEKEKORWSDNQSSGKDNYSIKEKEPEETMPKDRBEEBEEBLLKWMRICHSEN 420
XX	DR WPI: 2005-512270/52.	PR	421 YVSSDMDQVQDSTVGTSLRDLKDFEEBLGSIQVAKAARPPWEPKTYKLSDLESS 480
DR	N-PSDB; AEB47410.	PR	481 SESECESDEDSTCSSLSSDSEVFDVIAEIKKKKAHDRLHBLWYDQGQMDPLCKSA 540
DR	GENBANK; AAF80558.	PR	481 SESECESDEDSTCSSLSSDSEVFDVIAEIKKKKAHDRLHBLWYDQGQMDPLCKSA 540
XX	Use of RNase III for eliciting modification of a selected RNA target, promoting gene silencing of a gene, inhibiting the expression of a gene, or eliciting modification of an RNA target.	PR	541 KARRTGIRHSYYPEAKICCRPMINAGLPHYRITVSPPNFIJDRPTVIEHDYI 600
PT	Claim 19; SEQ ID NO 2; 32pp; English.	PR	541 KARRTGIRHSYYPEAKICCRPMINAGLPHYRITVSPPNFIJDRPTVIEHDYI 600
PT	The present invention relates to ribonuclease III (RNase III) nucleic acids and their encoding proteins. RNase III is an endoribonuclease that cleaves double stranded RNA. The invention is useful for eliciting modification of a selected RNA target in a cell, promoting gene silencing of a gene, inhibiting the expression of a gene, promoting modification of a gene and eliciting modification of a RNA target in a cell. The present sequence is human ribonuclease III (RNase III) protein.	PR	601 FEGFSMFAHAPLTLNIPLCVKYRNFNTYDITFTEEMPPENICVKGLBLFLSLFLFRDILEY 660
PT	XX	Db	601 FEGFSMFAHAPLTLNIPLCVKYRNFNTYDITFTEEMPPENICVKGLBLFLSLFLFRDILEY 660
PS	XX	Db	661 DWNLKGPLFEDSPPPCPFHMFRPFLPFLDGGKEVLSMHOIILYLRSCKALVBEETIA 720
PS	XX	Db	661 DWNLKGPLFEDSPPPCPFHMFRPFLPFLDGGKEVLSMHOIILYLRSCKALVBEETIA 720
PS	XX	Db	721 NMLQWELEWVKYAECKGMVTPCITPSAVRILDQDFRNPDVITPFLVHCGIRPA 780
PS	XX	Db	721 NMLQWELEWVKYAECKGMVTPCITPSAVRILDQDFRNPDVITPFLVHCGIRPA 780
PS	XX	Db	781 OLSYAGDPQOKLWKVSKYKUHLANSPKVQTKDOKLAQKREALQKIRQKNTMRREVTV 840
PS	XX	Db	781 OLSYAGDPQOKLWKVSKYKUHLANSPKVQTKDOKLAQKREALQKIRQKNTMRREVTV 840
PS	XX	Db	841 ELSQCFWKTCGIRSPVQCHAMLPVLTHTHRYQHCLMFLDKLIGYFQDRFLQMLQMLTHP 900
PS	XX	Db	841 ELSQCFWKTCGIRSPVQCHAMLPVLTHTHRYQHCLMFLDKLIGYFQDRFLQMLQMLTHP 900
CC	The present invention relates to ribonuclease III (RNase III) nucleic acids and their encoding proteins. RNase III is an endoribonuclease that cleaves double stranded RNA. The invention is useful for eliciting modification of a selected RNA target in a cell, promoting gene silencing of a gene, inhibiting the expression of a gene, promoting modification of a gene and eliciting modification of a RNA target in a cell. The present sequence is human ribonuclease III (RNase III) protein.	CC	901 SHHNGMNPARNLSNCGRCYQGDRKHMKKGINTLIMMSLQDPTPS 960
CC	CC	CC	901 SHHNGMNPARNLSNCGRCYQGDRKHMKKGINTLIMMSLQDPTPS 960
CC	CC	CC	961 RINHNERLREFGDAVVEFTSVHLYLFPSSLEGGIATYTAIVONHMLAKKELDP 1020
CC	CC	CC	961 RINHNERLREFGDAVVEFTSVHLYLFPSSLEGGIATYTAIVONHMLAKKELDP 1020

QY 1021 FMYLHAGPDLCESDLRHAMANCFEALIGAVLGSLEAKOLFGRLLNPDLEWMN 1080

Db 1021 FMYLHAGPDLCESDLRHAMANCFEALIGAVLGSLEAKOLFGRLLNPDLEWMN 1080

QY 1081 YPLHPLQLOQERTDROLIETSPVLOQKUTEFEERIAIGVIFTHYVRLARAFTRTGFNHLTL 1140

Db 1081 YPLHPLQLOQERTDROLIETSPVLOQKUTEFEERIAIGVIFTHYVRLARAFTRTGFNHLTL 1140

QY 1141 GHQRHEFLGIGSIMOLVATEYVIFHRDHESCHLTURSSUNRTOAKVSELGMOEA 1200

Db 1141 GHQRHEFLGIGSIMOLVATEYVIFHRDHESCHLTURSSUNRTOAKVSELGMOEA 1200

QY 1201 ITNDKTKRPGVIRTKLADLIESFIAIYTDILEXVHTFMVCFPRKKEFILNDWND 1260

Db 1201 ITNDKTKRPGVIRTKLADLIESFIAIYTDILEXVHTFMVCFPRKKEFILNDWND 1260

QY 1261 PMSQOCCLTRTEGEKPDIFPLYKLTQTVGSHARTYTAVYFKERRIGGGKPSIQA 1320

Db 1261 PMSQOCCLTRTEGEKPDIFPLYKLTQTVGSHARTYTAVYFKERRIGGGKPSIQA 1320

QY 1321 ENGAAMDALEKYNFPOWAHQKPIGKRYQELKEMMWEREIQEREDETEIKK 1374

Db 1321 ENGAAMDALEKYNFPOWAHQKPIGKRYQELKEMMWEREIQEREDETEIKK 1374

QY 61 TTFNSNAPRNELPPDFVPPRPPMPSAQAPLPPRPIRPPPNHQMRHPPVPPCPMPM 120

Db 61 TTFNSNAPRNELPPDFVPPRPPMPSAQAPLPPRPIRPPPNHQMRHPPVPPCPMPM 120

QY 121 PPPMPCDNPPVAGPAGPQGTPPPMMPSPSMHPPPPPMPOQVNQYPPGYSHNWPP 180

Db 121 PPPMPCDNPPVAGPAGPQGTPPPMMPSPSMHPPPPPMPOQVNQYPPGYSHNWPP 180

QY 181 SENFSNPNSSFLPSANNSSSPFRHLPYPLPKAPSERRSERPERLKHYDDHRHDSGR 240

Db 181 SENFSNPNSSFLPSANNSSSPFRHLPYPLPKAPSERRSERPERLKHYDDHRHDSGR 240

QY 241 GERRHSRDRRGRSPDRRDRDYSRDRGTRPDRHRSRERERHRHRSR 300

Db 241 GERRHSRDRRGRSPDRRDRDYSRDRGTRPDRHRSRERERHRHRSR 300

QY 301 PSLRSYKKEYRGSGSAGLGSVWPEPACTBLGETIKNTDSWAPLEIYHRSREK 360

Db 301 PSLRSYKKEYRGSGSAGLGSVWPEPACTBLGETIKNTDSWAPLEIYHRSREK 360

QY 361 KARWEREKEDRMSDNQSSGKDKNTSTKEKEPBTMDDKNEEEEEEELKPVWICHTSEN 420

Db 361 KARWEREKEDRMSDNQSSGKDKNTSTKEKEPBTMDDKNEEEEEEELKPVWICHTSEN 420

QY 421 YVSSPDKMQEDSTVYGTSDRDLYKFEELSGSROBKAARPPWEPKTKLDELESS 480

Db 421 YVSSPDKMQEDSTVYGTSDRDLYKFEELSGSROBKAARPPWEPKTKLDELESS 480

QY 481 SESCECSDEDSTCSSSSDSEPVDAIEKRRGKHPRLDLSWYDNPQMDGPKCSA 540

Db 481 SESCECSDEDSTCSSSSDSEPVDAIEKRRGKHPRLDLSWYDNPQMDGPKCSA 540

QY 541 KARRTGHRSTVYGEAEAKKPCPMTNTAGRLPHYRITVSPPTNFLTDRPTVTEYDDEYI 600

Db 541 KARRTGHRSTVYGEAEAKKPCPMTNTAGRLPHYRITVSPPTNFLTDRPTVTEYDDEYI 600

QY 601 PEGFSMFAHPLTNIPCKVIRFNIDTIEEMMPENFCVKGELPSLFLRDLLEY 660

Db 601 PEGFSMFAHPLTNIPCKVIRFNIDTIEEMMPENFCVKGELPSLFLRDLLEY 660

QY 661 DWNLKGPLFEDSPCCPRFHMPRFRLPDPGKEVLSMHQILLYLURCSKALVPEBIA 720

Db 661 DWNLKGPLFEDSPCCPRFHMPRFRLPDPGKEVLSMHQILLYLURCSKALVPEBIA 720

QY 721 NMLQWEEBLWQKVAECKGMIVTNPGKTPKSSVRIDQLDREQNPFDVITFPIVHFGIRPA 780

Db 721 NMLQWEEBLWQKVAECKGMIVTNPGKTPKSSVRIDQLDREQNPFDVITFPIVHFGIRPA 780

QY 781 OLSYAGDPPQYOKLWKSOKHLLANSPKVSKTOKLQARBEALKRQKNTMRSYTV 840

Db 781 OLSYAGDPPQYOKLWKSOKHLLANSPKVSKTOKLQARBEALKRQKNTMRSYTV 840

QY 841 ELSQGKWWKTGIRSDVQHAMMLPVLTTHYHQCLMHLKLGITYFQDCLLQAMTHP 900

Db 841 ELSQGKWWKTGIRSDVQHAMMLPVLTTHYHQCLMHLKLGITYFQDCLLQAMTHP 900

QY 841 ELSQGKWWKTGIRSDVQHAMMLPVLTTHYHQCLMHLKLGITYFQDCLLQAMTHP 900

Db 841 ELSQGKWWKTGIRSDVQHAMMLPVLTTHYHQCLMHLKLGITYFQDCLLQAMTHP 900

QY 901 SHLNFGNPDRHANSLSNCGTRQPKYGRKHMAMRKKGNTINLIMSLGQDPTPS 960

Db 901 SHLNFGNPDRHANSLSNCGTRQPKYGRKHMAMRKKGNTINLIMSLGQDPTPS 960

CC specification per se but was submitted in CD format by the inventor.

XX

SQ Sequence 1374 AA;

Query Match 99.8%; Score 7486; DB 8; Length 1374;

Best Local Similarity 99.9%; Pred. No. 0; Mismatches 2; Indels 0; Gaps 0;

Matches 1372; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 MMQGNITCRMSFHPGRGCCPRGRGGHGAAPSAFSFRPONRLIHPQQPVQYQEPPSAPS 60

Db 1 MMQGNITCRMSFHPGRGCCPRGRGGHGAAPSAFSFRPONRLIHPQQPVQYQEPPSAPS 60

QY 61 TTFNSNAPRNELPPDFVPPRPPMPSAQAPLPPRPIRPPPNHQMRHPPVPPCPMPM 120

Db 61 TTFNSNAPRNELPPDFVPPRPPMPSAQAPLPPRPIRPPPNHQMRHPPVPPCPMPM 120

QY 121 PPPMPCDNPPVAGPAGPQGTPPPMMPSPSMHPPPPPMPOQVNQYPPGYSHNWPP 180

Db 121 PPPMPCDNPPVAGPAGPQGTPPPMMPSPSMHPPPPPMPOQVNQYPPGYSHNWPP 180

QY 181 SENFSNPNSSFLPSANNSSSPFRHLPYPLPKAPSERRSERPERLKHYDDHRHDSGR 240

Db 181 SENFSNPNSSFLPSANNSSSPFRHLPYPLPKAPSERRSERPERLKHYDDHRHDSGR 240

QY 241 GERRHSRDRRGRSPDRRDRDYSRDRGTRPDRHRSRERERHRHRSR 300

Db 241 GERRHSRDRRGRSPDRRDRDYSRDRGTRPDRHRSRERERHRHRSR 300

QY 301 PSLRSYKKEYRGSGSAGLGSVWPEPACTBLGETIKNTDSWAPLEIYHRSREK 360

Db 301 PSLRSYKKEYRGSGSAGLGSVWPEPACTBLGETIKNTDSWAPLEIYHRSREK 360

QY 361 KARWEREKEDRMSDNQSSGKDKNTSTKEKEPBTMDDKNEEEEEEELKPVWICHTSEN 420

Db 361 KARWEREKEDRMSDNQSSGKDKNTSTKEKEPBTMDDKNEEEEEEELKPVWICHTSEN 420

QY 421 YVSSPDKMQEDSTVYGTSDRDLYKFEELSGSROBKAARPPWEPKTKLDELESS 480

Db 421 YVSSPDKMQEDSTVYGTSDRDLYKFEELSGSROBKAARPPWEPKTKLDELESS 480

QY 481 SESCECSDEDSTCSSSSDSEPVDAIEKRRGKHPRLDLSWYDNPQMDGPKCSA 540

Db 481 SESCECSDEDSTCSSSSDSEPVDAIEKRRGKHPRLDLSWYDNPQMDGPKCSA 540

QY 541 KARRTGHRSTVYGEAEAKKPCPMTNTAGRLPHYRITVSPPTNFLTDRPTVTEYDDEYI 600

Db 541 KARRTGHRSTVYGEAEAKKPCPMTNTAGRLPHYRITVSPPTNFLTDRPTVTEYDDEYI 600

QY 601 PEGFSMFAHPLTNIPCKVIRFNIDTIEEMMPENFCVKGELPSLFLRDLLEY 660

Db 601 PEGFSMFAHPLTNIPCKVIRFNIDTIEEMMPENFCVKGELPSLFLRDLLEY 660

QY 661 DWNLKGPLFEDSPCCPRFHMPRFRLPDPGKEVLSMHQILLYLURCSKALVPEBIA 720

Db 661 DWNLKGPLFEDSPCCPRFHMPRFRLPDPGKEVLSMHQILLYLURCSKALVPEBIA 720

QY 721 NMLQWEEBLWQKVAECKGMIVTNPGKTPKSSVRIDQLDREQNPFDVITFPIVHFGIRPA 780

Db 721 NMLQWEEBLWQKVAECKGMIVTNPGKTPKSSVRIDQLDREQNPFDVITFPIVHFGIRPA 780

QY 781 OLSYAGDPPQYOKLWKSOKHLLANSPKVSKTOKLQARBEALKRQKNTMRSYTV 840

Db 781 OLSYAGDPPQYOKLWKSOKHLLANSPKVSKTOKLQARBEALKRQKNTMRSYTV 840

QY 841 ELSQGKWWKTGIRSDVQHAMMLPVLTTHYHQCLMHLKLGITYFQDCLLQAMTHP 900

Db 841 ELSQGKWWKTGIRSDVQHAMMLPVLTTHYHQCLMHLKLGITYFQDCLLQAMTHP 900

QY 841 ELSQGKWWKTGIRSDVQHAMMLPVLTTHYHQCLMHLKLGITYFQDCLLQAMTHP 900

Db 841 ELSQGKWWKTGIRSDVQHAMMLPVLTTHYHQCLMHLKLGITYFQDCLLQAMTHP 900

QY 901 SHLNFGNPDRHANSLSNCGTRQPKYGRKHMAMRKKGNTINLIMSLGQDPTPS 960

Db 901 SHLNFGNPDRHANSLSNCGTRQPKYGRKHMAMRKKGNTINLIMSLGQDPTPS 960

CC current sequence is that of a human soft tissue sarcoma-upregulated protein of the invention. The current sequence is not shown within the

Sequence	99.8%; Score 7486; DB 9; Length 1374;
QY	Query Match Best Local Similarity 99.9%; Score 7486; DB 9; Length 1374; Matches 1372; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db	1021 FMLVYHGPDLCRESLRHAMANCFALIGAVLBSLEAKOLFGRLLFDPLREWLW 1080
Db	1021 FMLVYHGPDLCRESLRHAMANCFALIGAVLBSLEAKOLFGRLLFDPLREWLW 1080
QY	1 1081 YPLHLQLOPENTDQOLIESPVIQULTEBEAISVIFTRVLLRAFTRTVFNHLT 1140
Db	1081 YPLHLQLOPENPDQOLIESPVIQULTEBEAISVIFTRVLLRAFTRTVFNHLT 1140
QY	1 1141 GHNQMEFLGSIMQVATEYLIFIPDHNGHLTILRSSLUNNTQAKVABEGLGQVEYA 1200
Db	1141 GHNQMEFLGSIMQVATEYLIFIPDHNGHLTILRSSLUNNTQAKVABEGLGQVEYA 1200
QY	1 1201 ITNDKTKRPLVLTQKTLADLIESFTALYTKDQEYVHTFMVCFPRLKEFILNQDWN 1260
Db	1201 ITNDKTKRPLVLTQKTLADLIESFTALYTKDQEYVHTFMVCFPRLKEFILNQDWN 1260
QY	1 1261 PKSQOQCCULTRSGKEPDPLVKTLOQPSHARTYTAVFGKERICGGKGSQIA 1320
Db	1261 PKSQOQCCULTRSGKEPDPLVKTLOQPSHARTYTAVFGKERICGGKGSQIA 1320
QY	1 1321 EMGAANDALEKYNPPOMAHOKRFTGSKYRBLKEMWEREHOERDEDEDIK 1374
Db	1321 EMGAANDALEKYNPPOMAHOKRFTGSKYRBLKEMWEREHOERDEDEDIK 1374
RESULT 5	
ID ADVY17386	standard; protein; 1374 AA.
AC	ADYV17386;
DT	05-MAY-2005 (first entry)
XX	PRO polypeptide SEQ ID NO 3192.
XX	Antinflammatory; Immune disorder; Dermatological; Immunosuppressive; KW
KW	Anti-rheumatic; Anti-arthritis; Osteopathic; Hemostatic; Antianemic; KW
KW	Antithyroid; Antidiabetic; Nephrotopic; CNT-Gen.; Hepatotropic; KW
KW	Viricide; Gastrointestinal; Antipsoriatic; Anti-inflammatory; KW
KW	Antiallergic; db; gene; diagnosis; KW
OS	Homo sapiens.
XX	WO2005016962-A2.
XX	24 - FEB - 2005.
XX	PP 11-AUG-2004; 2004WO-US026249.
XX	11-AUG-2003; 2003US-0493546P.
PA	(GETH ) GENENTECH INC.
XX	Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;
PT	WPI; 2005-182330/19.
XX	New nucleic acid encoding PRO polypeptide, useful for diagnosing and
PT	treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.
XX	Claim 8; SEQ ID NO 3192; 158pp; English.
CC	The invention relates to an isolated nucleic acid encoding a PRO polypeptide. The polypeptide, agonist or an antagonist, antibody, composition, and method are useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis. The present sequence represents a DNA encoding a PRO polypeptide.
CC	961 RINHNERLEFGDAVEFLTSVHLYLIFPSLEGGGLATYTAIVONQHMLAKKELDP 1030
CC	901 SHHLNGMNDHARLSLNGCIRQKYGDKVHMRKGINTLIMSLGQDPTP 960
CC	901 SHHLNGMNDHARLSLNGCIRQKYGDKVHMRKGINTLIMSLGQDPTP 960
PT	841 ELSQGQFWKQGTSRVDQHAMLPVTHIRYHOCMLDKLIGYTFDRCQLQAMTHP 900
PT	841 ELSQGQFWKQGTSRVDQHAMLPVTHIRYHOCMLDKLIGYTFDRCQLQAMTHP 900
PS	781 QLSYAGDPQYQKLGWSYVKLHLLANSPKYQDKQKLAEREAQKIQKNTMRETV 840
XX	781 QLSYAGDPQYQKLGWSYVKLHLLANSPKYQDKQKLAEREAQKIQKNTMRETV 840
XX	721 NMLQBELEKQYABECKGKMTVNGTKOSSVRDOLDRQENPVITFJLIVHGRPA 780
PT	721 NMLQBELEKQYABECKGKMTVNGTKOSSVRDOLDRQENPVITFJLIVHGRPA 780
DR	Db
QY	781 QLSYAGDPQYQKLGWSYVKLHLLANSPKYQDKQKLAEREAQKIQKNTMRETV 840
Db	781 QLSYAGDPQYQKLGWSYVKLHLLANSPKYQDKQKLAEREAQKIQKNTMRETV 840
QY	841 ELSQGQFWKQGTSRVDQHAMLPVTHIRYHOCMLDKLIGYTFDRCQLQAMTHP 900
Db	841 ELSQGQFWKQGTSRVDQHAMLPVTHIRYHOCMLDKLIGYTFDRCQLQAMTHP 900
QY	901 SHHLNGMNDHARLSLNGCIRQKYGDKVHMRKGINTLIMSLGQDPTP 960
Db	901 SHHLNGMNDHARLSLNGCIRQKYGDKVHMRKGINTLIMSLGQDPTP 960
QY	961 RINHNERLEFGDAVEFLTSVHLYLIFPSLEGGGLATYTAIVONQHMLAKKELDP 1020
Db	961 RINHNERLEFGDAVEFLTSVHLYLIFPSLEGGGLATYTAIVONQHMLAKKELDP 1020

QY 1021 FMYAHGPDLCEDSLRHAMANCPEALIGAVLGSLEAKOLPGRLLNPDLDREWLN 1080  
 CC ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1021 FMYAHGPDLCEDSLRHAMANCPEALIGAVLGSLEAKOLPGRLLNPDLDREWLN 1080  
 CC ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 1081 YPLHPLQLOQEPNTDROLIETSPVQKLTTEFERAIGAVLGHVFLVLLAFTLRTVGFNHLTL 1140  
 CC ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1141 GHQRHEFLGLSISMLQVATEYVIFHEDPHHECHTLRSSUNRNQAKVABLGHOYA 1200  
 CC ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1141 GHQRHEFLGLSISMLQVATEYVIFHEDPHHECHTLRSSUNRNQAKVABLGHOYA 1200  
 CC ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 1201 ITNDKIKRPGVGRKTIKLADLSPFIAIPLYTDLEYHTFMNCPPRLKEFLNQWD 1260  
 CC ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1201 ITNDKIKRPGVGRKTIKLADLSPFIAIPLYTDLEYHTFMNCPPRLKEFLNQWD 1260  
 CC ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 1261 PKSQLOQCLTRTTEGKEDPDLIYKTHQTVGSHARTYTVAVYFKGERIGCKGKPSIQA 1320  
 CC ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1261 PKSQLOQCLTRTTEGKEDPDLIYKTHQTVGSHARTYTVAVYFKGERIGCKGKPSIQA 1320  
 CC ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 1321 ENGAAMOLEAKNPFQMAHOKPFIGKRYQEK-KEMRWEREHEOREPDTEDIKK 1374  
 CC ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1321 ENGAAMOLEAKNPFQMAHOKPFIGKRYQEK-KEMRWEREHEOREPDTEDIKK 1374  
 CC ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 6

ID ABU63361 standard; protein: 1373 AA.  
 XX ABU63361;  
 AC  
 XX DT 18-SEP-2003 (first entry)  
 XX DB Human double stranded RNase, RNase III.  
 XX KW Human; enzyme; RNase III; double stranded RNase; RNA target; gene silencing.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 FT Misc-difference 18 /note= "Encoded by CGT"  
 FT Misc-difference 1211 /note= "Encoded by GCG"  
 FT Misc-difference 1345 /note= "Encoded by GAA"  
 PN US200304941-A1.  
 XX PD 06-MAR-2003.  
 XX PP 20-FEB-2002; 2002US-00079185.  
 XX PR 06-JUN-1995; 96US-00659440.  
 PR 06-JUN-1997; 97US-0087008.  
 PR 07-JAN-2000; 2000US-0047983.  
 PR 06-JUL-2001; 2001US-0090425.  
 XX PA (CROO/) CROOKE S. T.  
 XX PI Crooke ST;  
 XX DR WPI; 2003-521756/49.  
 DR N-PSDB; ACD27526.

Biliciting a modification of a selected RNA target in a cell, useful for promoting inhibition of gene expression in a cell, comprises contacting an RNA-like polynucleotide-RNA target duplex with a polypeptide having an RNA-like polynucleotide-RNA target duplex with a polypeptide having an

XX The invention relates to eliciting a modification of a selected RNA target in a cell comprises contacting an RNA-like polynucleotide-RNA target duplex with a polypeptide comprising an RNase III domain. Also included are promoting gene silencing in a cell, inhibiting the expression of a gene in a cell comprising employing the method of cited above, promoting inhibition of expression of a gene, a hybrid RNase III (comprising at least one domain from a human RNase III and at least one domain from an RNase III of an organism other than human) and a cell having enhanced RNase III activity over an activity exhibited by a second cell (where the second cell is not enriched with respect to the amount or activity of RNase III polypeptide). The method is useful for eliciting a modification of a selected RNA target in a cell, and for promoting inhibition of expression of a gene in a cell. Compositions comprising RNase III polypeptides or polynucleotides are useful for research, biological and clinical purposes. The polynucleotides are may be used in defining the roles of RNase III and the interaction of human RNase III and cellular RNA. Host cells can be used for the production of human RNase III and for identifying agents which increase or decrease levels of expression or activity of human RNase III in the cell. The present sequence represents human RNase III (a double stranded RNase)  
 XX SQ Sequence 1373 AA;  
 Query Match 99.8%; score 7483.5; DB 7; Length 1373;  
 Best Local Similarity 99.9%; Pred. No. 0; Mismatches 0; Indels 1; Gaps 1;  
 Matches 1373; Conservative 0;  
 CC 1 MMQGNTCHRMSTHPGRGCPGRGGHGGGARPSAPSFRPQNRLHMQQPWQYEPSSAPS 60  
 Db 1 MMQGNTCHRMSTHPGRGCPGRGGHGGGARPSAPSFRPQNRLHMQQPWQYEPSSAPS 60  
 QY 61 TTFNSNSPAPNPLPQPRDPDVFPPRPPMPPSAQGSLPPCPDRPPPNHQMRHPPFVPPCPM 120  
 Db 61 TTFNSNSPAPNPLPQPRDPDVFPPRPPMPPSAQGSLPPCPDRPPPNHQMRHPPFVPPCPM 120  
 QY 121 PRPPMPCNNPPVPGAPGQGTPFPPMPPSMPHPPPPMPPSMPHPPPPMPPVPGYSHHNPFP 180  
 Db 121 PRPPMPCNNPPVPGAPGQGTPFPPMPPMPPSMPHPPPPMPPVPGYSHHNPFP 180  
 QY 181 SFSNPQNPSSPLSANNSSSPHFPHIIPYPLPKASSESSRSERLKKYDHHRDHSGR 240  
 Db 181 SFSNPQNPSSPLSANNSSSPHFPHIIPYPLPKASSESSRSERLKKYDHHRDHSGR 240  
 QY 241 GHRHSLRREGRSPDRRQDRPSYRDRYDQDRGRTPSRSRSYRSRERERURHRDRRS 300  
 Db 241 GHRHSLRREGRSPDRRQDRPSYRDRYDQDRGRTPSRSRSRERERURHRDRRS 300  
 QY 301 PSLRSYKKEYGRGSGRGSGYGLSVPEPAGCTPELPGELIKNTLSSWAPPLEVHRSRSER 360  
 Db 301 PSLRSYKKEYGRGSGRGSGYGLSVPEPAGCTPELPGELIKNTLSSWAPPLEVHRSRSER 360  
 QY 361 KQARWEKEKDSDNQSGKDKNTSKEKEFETMDDKNEEEBELLKPKWIRCHSEN 420  
 Db 361 KQARWEKEKDSDNQSGKDKNTSKEKEFETMDDKNEEEBELLKPKWIRCHSEN 420  
 QY 420 YVSSDPMDQVGSTVVGTSRSLRDYDKEEEIGSROEKAARPPMPEPKTKLDELISS 480  
 Db 421 YVSSDPMDQVGSTVVGTSRSLRDYDKEEEIGSROEKAARPPMPEPKTKLDELISS 480  
 QY 481 SSEESEDEDSDTSSSDSESEVDVIAKIKKCAHPDHLDEWYDNGQMDGPLCKCSA 540  
 Db 481 SSEESEDEDSDTSSSDSESEVDVIAKIKKCAHPDHLDEWYDNGQMDGPLCKCSA 540  
 QY 541 KARRTGGRHSIYPGEEAKCPRTMNTNAGRFLHYRTVSPPINPLDRPTVIEYDHEYI 600  
 Db 541 KARRTGGRHSIYPGEEAKCPRTMNTNAGRFLHYRTVSPPINPLDRPTVIEYDHEYI 600  
 QY 601 FSGFSMPAHAPLNPICKVIRNIDYTHTEEMMPBNFCVKGLEIFSLFAPDRLILEY 660  
 Db 601 FSGFSMPAHAPLNPICKVIRNIDYTHTEEMMPBNFCVKGLEIFSLFAPDRLILEY 660  
 QY 661 DNLKGPFEDSPPCCPRFHMPRFVRLPDGKEVLSMHQIILYLLRCSKALVPEBEIA 720



QY	179	-----	178
347	PLEINHRSPSREKRARWBEKKDRNSDNQSSGKDKNTSIKEKEPEETMPDKNEEEEEE	406	
Db	-----		
179	-----SRSPSREKRARWBEKKDRNSDNQSSGKDKNTSIKEKEPEETMPDKNEEEEEE	232	
QY	407 LKKWVWRCRTHSEWYSSPMDQWDGSTDVGTSLRDYDKEFELGRQEKAKARPW	466	
Db	233 LKKWVWRCRTHSEWYSSPMDQWDGSTDVGTSLRDYDKEFELGRQEKAKARPW	292	
QY	293 EPPKTKDDESSSESESSESDESDSTCSCSSDSEFDVTAIEKRAKAHDRLADLWND	352	
Db	467 EPPKTKDDESSSESESSESDESDSTCSCSSDSEFDVTAIEKRAKAHDRLADLWND	526	
QY	527 PGQMDGPICKCSAKARRYGIRHSYYPGEAIKCRPMWNTAQRLFHRITVSPPTNLT	586	
Db	353 PGQMDGPICKCSAKARRYGIRHSYYPGEAIKCRPMWNTAQRLFHRITVSPPTNLT	412	
QY	567 DRPTVIEDHEYREGSMFALPLNIPCKURPNIDYTHIPESEMPPFCVKE	646	
Db	413 DRPTVIEDHEYREGSMFALPLNIPCKURPNIDYTHIPESEMPPFCVKE	472	
QY	647 LFSLPLFRDILEDLYDWNLKGPLFEDSPCCPREFMPFRVFLPDDGKSVLSEHQLYL	706	
Db	473 LFSLPLFRDILEDLYDWNLKGPLFEDSPCCPREFMPFRVFLPDDGKSVLSEHQLYL	532	
QY	707 LRCSKALVPEETANLQMELEVKYAAECKGMVTPGTKSSVRDQDREQFNDV	766	
Db	533 LRCSKALVPEETANLQMELEVKYAAECKGMVTPGTKSSVRDQDREQFNDV	592	
QY	767 ITFPIIVHGRPAQSYAGDPOQKLWSYKLRLJLANSKPKQTOKQKLAQREALQ	826	
Db	593 ITFPIIVHGRPAQSYAGDPOQKLWSYKLRLJLANSKPKQTOKQKLAQREALQ	652	
QY	827 KIRQNTMREBVTTELSSOGFWKIGIRSVCQHAMMLPTLTHIRYRCIMLHDKLIGYT	886	
Db	653 KIRQNTMREBVTTELSSOGFWKIGIRSVCQHAMMLPTLTHIRYRCIMLHDKLIGYT	712	
QY	887 FQDRCLLQAMTHSHHNLNGMNFDHARNSLSNCIGRQPKYGRKVKHMHMRKGINTLI	946	
Db	713 FQDRCLLQAMTHSHHNLNGMNFDHARNSLSNCIGRQPKYGRKVKHMHMRKGINTLI	772	
QY	947 NMSRLGQDPTPERINHNRLELGGDAVEFLJSHYVLPFSLBEGGLATRTAVON	1006	
Db	773 NMSRLGQDPTPSRINHNRLELGGDAVEFLJSHYVLPFSLBEGGLATRTAVON	832	
QY	1007 OHLAMLAKKLEDPFLYAHGPOLCRESDLRHAMANCEBALIGAVYLEGSLBEGQLFGR	1066	
Db	833 OHLAMLAKKLEDPFLYAHGPOLCRESDLRHAMANCEBALIGAVYLEGSLBEGQLFGR	892	
QY	1067 LLFNDPDRREVWLNYPHLPLQOBNTSRQLIETSPTVQQLTREFA1GIVFTHVRLAR	1126	
Db	893 LLFNDPDRREVWLNYPHLPLQOBNTSRQLIETSPTVQQLTREFA1GIVFTHVRLAR	952	
QY	1127 AFTLRTVGPNHLTGHNORMEFLGDSIMOLVATELFTHPDHGHHTLASSVNRT	1186	
Db	953 AFTLRTVGPNHLTGHNORMEFLGDSIMOLVATELFTHPDHGHHTLASSVNRT	1072	
QY	1118 QAKVUEBLGMOEATNDKTKRPVGLRKTTLADLLESTIALYDQDLYVHTFMNCFF	1246	
Db	1013 QAKVUEBLGMOEATNDKTKRPVGLRKTTLADLLESTIALYDQDLYVHTFMNCFF	1012	
QY	1247 PRUKFPLINQDNDPQPSQLQOCQCLTRTEGKEDPILYKLTQTVGSPHARTYTVAVYFGK	1306	
Db	1073 PRUKFPLINQDNDPQPSQLQOCQCLTRTEGKEDPILYKLTQTVGSPHARTYTVAVYFGK	1132	
QY	1307 ERIGGKGPSIQQEMGAMDALEKYNFQOMATOKRFTGRKQRCLEMWREREQREP	1366	
Db	1133 ERIGGKGPSIQQEMGAMDALEKYNFQOMATOKRFTGRKQRCLEMWREREQREP	1192	
QY	1367 DFTEDIKK 1374		

3  
 CC of a selected cellular RNA target and promoting RNA interference (RNAi)  
 CC in a cell. The RNase III polypeptide, the polynucleotide encoding it and  
 CC the antisense oligonucleotides, are useful for gene therapy (e.g. for  
 CC treating a disease or disorder associated with RNase III expression or  
 CC activity, or associated with an infectious agent), prophylaxis or  
 CC research reagents. The sequence presented is the human RNase III protein  
 XX  
 SQ Sequence 1374 AA:  
 Query Match 80.8%; Score 6062; DB 6; Length 1374;  
 Best Local Similarity 100.0%; Pred No. 0;  
 Matches 1101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MMQGNTCHMSRFPGRGCPGRGGCARSAPSFRPONTRLHPDQPPVQYQEPAPS 60  
 Db 274 MVOQNTCHMSRFPGRGCPGRGGCARSAPSFRPONTRLHPDQPPVQYQEPAPS 333  
 QY 61 TTFNSNPAVNLPDPDFVPPPPMPSAQCGLPPIPFPFPNQHMRHPPVPPCPFM 120  
 Db 334 TTFNSNPAVNLPDPDFVPPPPMPSAQCGLPPIPFPFPNQHMRHPPVPPCPFM 393  
 QY 121 PPPMPCPNNPPVPGAPPGQGTPPFMPPMPSMPPSHPPPPVPMQVNQYPPGSHNFP 180  
 Db 394 PFPMPCPNNPPVPGAPPGQGTPPFMPPMPSMPPSHPPPPVPMQVNQYPPGSHNFP 453  
 QY 181 SFNSRQNPPSFLPSANNSSSPFHRRHPPVPPCPF 240  
 Db 454 SFNSRQNPPSFLPSANNSSSPFHRRHPPVPPCPF 513  
 QY 241 GERRHSLDRRGRSDRRQDSRYSRDSYDGRGTRSRHSYVERSRRERERHRRHRR 300  
 Db 514 GERRHSLDRRGRSDRRQDSRYSRDSYDGRGTRSRHSYVERSRRERERHRRHRR 573  
 QY 301 PSLSRSYKKEYRSGRSYGSLSVPEPAGCTPEBLPGETIKNITDSWAPPLETVNHRSPREK 360  
 Db 574 PSLSRSYKKEYRSGRSYGSLSVPEPAGCTPEBLPGETIKNITDSWAPPLETVNHRSPREK 633  
 QY 361 KPARWEREKRDRWSNDSGKPNYTSIKEKEPEETMPDKEEEEEEELKPYWIRCHSEN 420  
 Db 634 KPARWEREKRDRWSNDSGKPNYTSIKEKEPEETMPDKEEEEEEELKPYWIRCHSEN 693  
 QY 421 YSSDDMDQVGSITWTSRDRDLYKFEELIGSRSQEKAKARPPWPKTKLDDLESS 480  
 Db 694 YSSDDMDQVGSITWTSRDRDLYKFEELIGSRSQEKAKARPPWPKTKLDDLESS 753  
 QY 481 SSECECSDEDSTCSSLSSDSEVFDVIAIKRKAHPDRLHDLYWYNDPGQMDGPICKSA 540  
 Db 754 SSECECSDEDSTCSSLSSDSEVFDVIAIKRKAHPDRLHDLYWYNDPGQMDGPICKSA 813  
 QY 541 KARRTGIRHSIYGEAIKPCPRMNTNAGRLHYRITVSPPNFLDRPTVIEYDHEYI 600  
 Db 814 KARRTGIRHSIYGEAIKPCPRMNTNAGRLHYRITVSPPNFLDRPTVIEYDHEYI 873  
 QY 601 FEGFSMFAHAPLTIICKVIRNFNIYTIHFLEEMBNFCKGKGLFSLFLFDILEY 660  
 Db 874 FEGFSMFAHAPLTIICKVIRNFNIYTIHFLEEMBNFCKGKGLFSLFLFDILEY 933  
 QY 661 DWNLKGFLFEDSPPPCCPRFHRMPFRFLPDGKEVLSMHQILYIARCSQVBBIA 720  
 Db 934 DWNLKGFLFEDSPPPCCPRFHRMPFRFLPDGKEVLSMHQILYIARCSQVBBIA 993  
 QY 721 NMLQWBLEWOKYAECKGMIYTPGKTPSSRIDOLEBDFNPDVITFPIVHRCIRPA 780  
 Db 994 NMLQWBLEWOKYAECKGMIYTPGKTPSSRIDOLEBDFNPDVITFPIVHRCIRPA 1053  
 QY 781 QLSYAGDPOYQOLKSYKUMLRLLANSKPKVQDKQKLAQFEEAQKIRONTMRETV 840  
 Db 1054 QLSYAGDPOYQOLKSYKUMLRLLANSKPKVQDKQKLAQFEEAQKIRONTMRETV 1113  
 QY 841 ELSQGEMWKTGJRSVQHAMMLPVLTHIRYHQCLMHDKLIGYFQDRCLQLMTHP 900  
 Db 1114 ELSQGEMWKTGJRSVQHAMMLPVLTHIRYHQCLMHDKLIGYFQDRCLQLMTHP 1173

QY 901 SHHLHFGMNDPHARNSLSNGCIRQKYGDKVHMMRKGINTLNMARLGQDPTS 960  
 Db 1174 SHHLHFGMNDPHARNSLSNGCIRQKYGDKVHMMRKGINTLNMARLGQDPTS 1233  
 QY 961 RINHNERLELTGDAVETLISVHLTYLPFLESGLATYTAIVONOHMLAKLKLBDP 1020  
 Db 1234 RINHNERLELTGDAVETLISVHLTYLPFLESGLATYTAIVONOHMLAKLKLBDP 1293  
 QY 1021 FMLYAHGPDLCRESDIRHMANCCEALIGAVLGSLEAKOLGRLLFUDPDLREWL 1080  
 Db 1294 FMLYAHGPDLCRESDIRHMANCCEALIGAVLGSLEAKOLGRLLFUDPDLREWL 1353  
 QY 1081 YPLHPLQLOQENTDQIETS 1101  
 Db 1354 YPLHPLQLOQENTDQIETS 1374

RESULT 9  
 AAB92635  
 ID AAB92635 standard; protein; 769 AA.  
 XX  
 AC AAB92635;  
 XX  
 DT 26-JUN-2001 (first entry)  
 XX  
 DE Human protein sequence SEQ ID NO:10949.  
 XX  
 KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1074617-A2.  
 XX  
 PD 07-FEB-2001.  
 XX  
 PR 28-JUL-2000; 2000EP-00116126.  
 XX  
 PR 29-JUL-1999; 99JP-00248036.  
 PR 27-AUG-1999; 99JP-00300253.  
 PR 11-JAN-2000; 2000JP-00118776.  
 PR 02-MAY-2000; 2000JP-00183767.  
 PR 09-JUN-2000; 2000JP-00241899.  
 XX  
 PA (HELI-) HELIX RES INST.  
 XX  
 PI Ota T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;  
 XX  
 DR WPI: 2001-318749/34.

XX  
 PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

XX  
 PS Claim 8; SEQ ID NO 10949; 2537pp + Sequence Listing; English.

CC The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises:  
 CC (a) an oligo-dT primer and an oligonucleotide complementary to the  
 CC complementary strand of a polynucleotide which comprises one of the 5602  
 CC nucleotide sequences defined in the specification, where the  
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
 CC of an oligonucleotide comprising a sequence complementary to the  
 CC complementary strand of a polynucleotide which comprises a 5'-end  
 CC sequence and an oligonucleotide comprising a sequence complementary to a  
 CC polynucleotide which comprises a 3'-end sequence, where the  
 CC oligonucleotide comprises at least 15 nucleotides and the combination of  
 CC the 5'-end sequence/3'-end sequence is selected from those defined in the  
 CC specification. The primer sets can be used in antisense therapy and in  
 CC gene therapy. The primers are useful for synthesising polynucleotides,  
 CC particularly full-length cDNAs. The primers are also useful for the  
 CC detection and/or diagnosis of the abnormality of the proteins encoded by

CC the full-length cDNAs. The primers allow obtaining of the full-length  
 CC cDNAs easily without any specialised methods. AAI0166 to AAI13628 and  
 CC AAI13633 to AAI18742 represent human cDNA sequences; AAB92445 to AAB93893  
 CC represent human amino acid sequences; and AAI13629 to AAI13622 represent  
 CC present invention  
 XX sequence 769 AA;

Query Match 54.3%; Score 4071; DB 4; Length 769;  
 Best Local Similarity 99.5%; Pred. No. 4, 2e-280; Mismatches 0; Indels 0; Gaps 0;  
 Matches 765; Conservative 0; MisMatches 4; Indels 0; Gaps 0;

DB 606 MPAHAPLTPNIPICKVIRENIDITIHFTEEMMPENPCVKGLEFSLFRDIDLYDNLK 665  
 1 MPAHAPLTPNIPICKVIRENIDITIHFTEEMMPENPCVKGLEFSLFRDIDLYDNLK 60  
 QY 666 GPLFEDSPCCPRFHMRVFLPFLDGKEVLSMHQILYLARCSKALVPEERIANNLQW 725  
 61 GPLFEDSPCCPRFHMRVFLPFLDGKEVLSMHQILYLARCSKALVPEERIANNLQW 725  
 Db 726 ELEWQKAYAEECKGMIVNPGKPSYRIDLQREQENPDVTPPTIIVHFGGRPAOLSYA 785  
 121 ELEWQKAYAEECKGMIVNPGKPSYRIDLQREQENPDVTPPTIIVHFGGRPAOLSYA 180  
 QY 786 GPQYQKULKSYKLUHLANSRKYQTDQKQLAQREBALQIKRQKOMRREUTVLSQ 845  
 181 GPQYQKULKSYKLUHLANSRKYQTDQKQLAQREBALQIKRQKOMRREUTVLSQ 240  
 QY 846 GPKTGTRSDVQHAMMLPVLTHHTRYHOCMHLKLGTYTQDRCLQIQLAMTHPSHLN 905  
 241 GPKTGTRSDVQHAMMLPVLTHHTRYHOCMHLKLGTYTQDRCLQIQLAMTHPSHLN 905  
 Db 906 RSKNPDHARNLSNSCGRQPKGDRKVHMHHMKKGINTLNNMSRIGQDQDTPSRINH 965  
 906 RSKNPDHARNLSNSCGRQPKGDRKVHMHHMKKGINTLNNMSRIGQDQDTPSRINH 965  
 Db 301 RSKNPDHARNLSNSCGRQPKGDRKVHMHHMKKGINTLNNMSRIGQDQDTPSRINH 360  
 QY 966 ERLEFLGDAWVEFTLWVLYYQPSLREGGLATRTAVQNHLMJAKKLDPMIYA 1025  
 361 ERLEFLGDAWVEFTLWVLYYQPSLREGGLATRTAVQNHLMJAKKLDPMIYA 420  
 QY 1026 HGDPLCRESDRHARNAMCFAELIGAVVLEGSLBEAKQLGRILFNDPDLREWLNYLHP 1085  
 421 HGDPLCRESDRHARNAMCFAELIGAVVLEGSLBEAKQLGRILFNDPDLREWLNYLHP 480  
 Db 1086 LQLEPNTDROLIETSPYQKLTPEEEAIGVYPTFHVLARAPLRTWGENHTLGNQR 1145  
 1086 LQLEPNTDROLIETSPYQKLTPEEEAIGVYPTFHVLARAPLRTWGENHTLGNQR 1145  
 Db 481 LQLEPNTDROLIETSPYQKLTPEEEAIGVYPTFHVLARAPLRTWGENHTLGNQR 540  
 QY 1146 MERLGDSTMOLVATEYLHFPDHHEGLTLIASSLNUVRTAKVABELGMOEYATNDK 1205  
 541 MFLGLDSIMOLVATEYLHFPDHHEGLTLIASSLNUVRTAKVABELGMOEYATNDK 600  
 QY 1206 TKEPVGLRKTTLADLLESPITALYTDKOLEYVTEEMNCFFPLRKEFTLNDQNDPKSQL 1265  
 601 TKEPVGLRKTTLADLLESPITALYTDKOLEYVTEEMNCFFPLRKEFTLNDQNDPKSQL 660  
 Db 1266 QQQCLTRTTEGKEDPIYKLTQTVGSHARTTYWVYFKGRIGCKGKGPSTQQAENGAA 1325  
 661 QQQCLTRTTEGKEDPIYKLTQTVGSHARTTYWVYFKGRIGCKGKGPSTQQAENGAA 720  
 QY 1326 MALEKKNPOMAHQKPIGRKQYQELKEMMRREHOREREPPTEDIKK 1327  
 721 MALEKKNPOMAHQKPIGRKQYQELKEMMRREHOREREPPTEDIKK 769  
 Result 10  
 ABB5839 ID ABB5839 standard; protein; 1327 AA.  
 XX ' ABB5839;  
 AC ABB5839;  
 XX DT 26-MAR-2002 (first entry)

DB 3 QPLPLPPPPVQPA-----PPPPPPPPSDELSLSPGVGVPSHVNNSNSHSQ 46  
 QY 138 GQGTFPEMPPPSPMPPHPPPPVMPQDVNYQYQPGY-----SHNFP 179  
 47 SSKLSDVYVTPETPAPVSS--VPSVSYQQPQPAYGVEGYAVNEQAKYKGSGEBSHQYQ 103  
 Db 180 PSRNFSQNPSSPLPSANNSSSPHRFLPPYPL---PKAPRSRSRPERLKHDDHRRD 235  
 QY 104 PA-----SGSSEFLYES-----YKDFDRYPAVSSNRPSSERQ-----RTS 139  
 Db 236 HSGRGRBRSRDRRGRSPDRRQDSRYSRDSYDRGRTPSRHSRSRERERURHR 295  
 QY 140 NSSQGTHYP-----GYSSGR-----RYEQRHDQ---BHQIQDPSRYAHEPHGHY 183  
 296 DNRSPSLESYKKEYKRSGRSGSYGLSVPERAGCTPBLGEITKNTDSWAPPLETIVHRS 355  
 Db 184 AHRQAKSSQHGT---YQSSARN-----QVSDDYSPRGHHERP 219  
 QY 356 PSREKKKA-RHEBEKDR---WSDNOSGKDKNNTSIKEKEPEETMPDKNEEEBLK 409  
 Db 220 ETELETRKPKVETERDRILLRQCSNFC-----BKEPDYKMKMNLSEADAPV 267  
 QY 410 PWIRCTHSNTYSSDDMDQEDSTVGTGSRILDVKKEELGSROKAKARPPWEP 469

QY	470 KTKL-----DEDLESSESCEPESDSTCSCSSSDSEVFV-----IAEIKKKAH 514	DT	22-SEP-2003 (first entry)
Db	324 PRKARRVCKGHKHKSEACSSSSSDSDSDEA-----FKEQDCMEEILSRKVQH 373	DE	Human putative ribonuclease III.
QY	515 PDRLELDELWNTDPGCNDGFLCKCSAKARSTGIRSHYIYGPBEATKPCRDMTNNAQGLFHY 574	XX	
Db	374 PQRVHADLNHNDAGEGMNDGFLCRCGAKSRIGIRGIGIYFEGTGYKLCDPNSNNWAGKLFHY 433	KW	spinal cord; neuropathic pain; central sensitisation pain; pain; analgesic; gene therapy.
QY	575 RITVSPPTNLTDRIVTDHEYIFEGSMPMAHAPLNTPLUCKVIRNIDYHPTEE 634	XX	
Db	434 RISIISPTNLTKTTPTIKDHEBFLPEGISLSSVRLSLPVCKVIRNEYIETEYE 493	OS	Homo sapiens.
QY	635 MMPENPCVKCQLEFLSSLFRDILEYDWNJKGPL---FEDSPPCCPREHFMFRFVFLP 690	XX	
Db	494 KMPENFTIHLDDIFFKYLFLFELLEVDENMPNPSGNTES---CPATHFPRFVFLP 550	XX	
QY	691 DGGKEVVLMSHQILLYLRLRSKALVVEEETAMLOVEELEMQVAKBECKAMIVTNGTAKS 750	XX	
Db	551 DNGKEVVLAMWEVRLYILDNSAQVLERQQLAHNQTSQSEWQNYVDFIKGMLVNTKEGYKPC 610	XX	
QY	751 SVRITDOLDREROFNPY-----ITPITVHICRPAQLSPYAGDPOVQLWKSYYKLR 801	XX	
Db	611 SLRVVOLDRN-NSLSPCVDRETGTSRPAVHICRPAQLSPYAGDPOVQLWKSYYKLR 668	XX	
QY	802 HLLANSPLSPKVQQTDKOQLAQREALQKQNTMREBVTELSSOCFWKTCIRSDWCQHAM 861	XX	
Db	669 HLMAMTSKOSFKDKKQKLEKEQKQIYQEMRQGRMKNTVIAISSEGGFVYRGMCDVQHAM 728	XX	
QY	862 MLPVTHITRHYQCMNHLDKLIGYTFQDRCLLQQLAMTHPSHHLNGFMNDHARNLNSNG 921	XX	
Db	729 LIPITGTHLRFHKSQDLLEDESIGFRKRNRYLQLLTHFSYKENGTFNHDHARNLNTG 788	XX	
QY	922 IROPCYGDVKHMMRKKGKINTLNIMSLGODDPTPERINHFERLETFIDAVWEFTS 981	XX	
Db	789 IROPCYGDVKHMMRKKGKINTLNIMSLGODDPTPERINHFERLETFIDAVWEFTS 848	XX	
QY	982 VHLVYLPSPLEGGATYRATIVQHQLAMAKKULDPMLYAHGPDLICRESDLRHAM 1041	XX	
Db	849 IHLFFMPPELEEGGATYRATIVQHQLAMAKKULDPMLYAHGPDLICRESDLRHAM 908	XX	
QY	1042 NCFEALIGAVYLEGLESLEAKQLGFLF-NDPDIREVWLNYPHLPLQLOQEPNTRDQLIET 1100	XX	
Db	909 NCFEALMGALLDGGIKADEVFTDLPFRODEKULSIWQKULPERLQOEPGLGDSIDS 968	XX	
QY	1101 SPVQKQLTTEFEATGVTFTVRLRAFTRTVGNPLHTGHNGRMERFEGDSTMOLVATE 1160	XX	
Db	969 YRVKELTKEDSTQKFKRILKRAFTRSIGHTLTLGSNQRLREFGDTVQQLICSE 1028	XX	
QY	1161 YLFHPPDHHEGHLTLLRSVNNNTQAKVABEGLGQMEVAT-TNDKTKPVGARTKTLAD 1219	XX	
Db	1029 YLYRIFPEHHEGHLSLRLRSVNNNTQAVYCDLGMPPKAVYANBK---ADLKTKDRA 1084	XX	
QY	1220 LLESTITALYTDKOLEYVHTFMNCVFFPRKEFTINLQDNNDPQSQQCLTART-EGKE 1278	XX	
Db	1085 LLEARFLGALYDKGGLYCEOFCHVOLPFLQFLINQMDNDPQSKLQOCCLTRT-EGKE 1144	XX	
QY	1279 PDIPIYKLTGTVGSSHARTTYVAFVFKGERIGCGKGPSQQAENGAMDALEKN--PQ 1336	XX	
Db	1145 PDIPIYKUVASGPNTTRVKAVFRSKLATSSGSSQQAENGAMDALEKN--PQ 1204	XX	
QY	1337 MAHQKFRIGKRYQRL--KEMRWREREHOREPDETEIKK 1374	XX	
Db	1205 LDHQQRVIANSIKKPTGNELDNDSPRQHQE----EKIKR 1239	XX	
RESULT 11			
ID ABM04841	ABM04841 standard; protein; 541 AA.		
AC ABM04841:			

QY	1334	GPSIQQAEMGAAANDALEKYNPQMAHQKRFIGKRYQQLKEMWEREHOEREPDEDEDIK	1373
Db	481	GPSIQQAEMGAAANDALEKYNPQMAHQKRFIGKRYQQLKEMWEREHOEREPDEDEDIK	540
QY	1374	K 1374	
Db	541	K 541	
AC		AEA21037;	
XX			
DT	11-AUG-2005	(first entry)	
DE	Novel human polypeptide SEQ ID NO 1731.		
XX			
KW	vulnerary; CNS-gen.; gene therapy; diagnostic; forensic; mapping; DNA purification; protein purification; osteoarthritis; antirheumatic; osteopathic; musculoskeletal disease; osteoporosis; endocrine disease; periodontal disease; antiinflammatory; mouth disease; burns; injury; peripheral neuropathy; Alzheimer's disease; neuroprotective; nociceptive; degeneration; parkinsons disease; antiparkinsonian; neurological disease; cerebrovascular ischemia; cerebroprotective; vasotrophic; cardiovascular disease; autoimmune disease; immunosuppressive; immune disorder; viral infection; viricide; infection; cancer; cytotoxic; neoplasm.		
OS	Homo sapiens.		
XX			
PN	WO2005049806-A2.		
XX			
PD	02-JUN-2005.		
XX			
PP	11-MAR-2004; 2004WO-US007412.		
XX			
PR	14-MAR-2003; 2003US-00389559.		
XX			
PA	(NUVE-) NUVELO INC.		
XX			
PI	Tang TY, Wang J, Zhang J, Ren F, Zhou P, Ma Y; Ghosh M, Xie A, Asundi V, Zhao Q, Wang D, Goodrich R, Chen R; Wehrman T, Weng G, Boyle B; WPI; 2005-417730/42.		
XX			
PT	New polynucleotide encoding a polypeptide with biological activity, useful for treating a disease or disorder, e.g., osteoarthritis, burns, CNS and peripheral disease, stroke, autoimmune disorders, viral infection, or cancer.		
PT			
PS	Example 3; SEQ ID NO 1731; 500pp; English.		
XX			
CC	The invention describes a new isolated polynucleotide (I) encoding a polypeptide with biological activity comprising: a nucleotide sequence of SEQ ID NOS: 1-567 (fully defined); a nucleotide sequence that hybridizes to the sequence of (1) under stringent hybridization conditions; or a nucleotide sequence having greater than 99% sequence identity with the sequence of (1). Also described are: a(n) (expression) vector comprising (I); a host cell genetically engineered to comprise (I) operatively, associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell; an isolated polypeptide comprising a sequence of SEQ ID NOS: 568-1134 (fully defined), where the polypeptide is: a polypeptide encoded by (I); or a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NOS: 1-567; a composition comprising the polypeptide of (3) and a		
RESULT 12			
AEA21037	standard; protein; 486 AA.		
XX			
AC	AEA21037;		
XX			
DT	11-AUG-2005 (first entry)		
DE	Novel human polypeptide SEQ ID NO 1731.		
XX			
KW	vulnerary; CNS-gen.; gene therapy; diagnostic; forensic; mapping; DNA purification; protein purification; osteoarthritis; antirheumatic; osteopathic; musculoskeletal disease; osteoporosis; endocrine disease; periodontal disease; antiinflammatory; mouth disease; burns; injury; peripheral neuropathy; Alzheimer's disease; neuroprotective; nociceptive; degeneration; parkinsons disease; antiparkinsonian; neurological disease; cerebrovascular ischemia; cerebroprotective; vasotrophic; cardiovascular disease; autoimmune disease; immunosuppressive; immune disorder; viral infection; viricide; infection; cancer; cytotoxic; neoplasm.		
OS	Homo sapiens.		
XX			
PN	WO2005049806-A2.		
XX			
PD	02-JUN-2005.		
XX			
PP	11-MAR-2004; 2004WO-US007412.		
XX			
PR	14-MAR-2003; 2003US-00389559.		
XX			
PA	(NUVE-) NUVELO INC.		
XX			
PI	Tang TY, Wang J, Zhang J, Ren F, Zhou P, Ma Y; Ghosh M, Xie A, Asundi V, Zhao Q, Wang D, Goodrich R, Chen R; Wehrman T, Weng G, Boyle B; WPI; 2005-417730/42.		
XX			
PT	New polynucleotide encoding a polypeptide with biological activity, useful for treating a disease or disorder, e.g., osteoarthritis, burns, CNS and peripheral disease, stroke, autoimmune disorders, viral infection, or cancer.		
PT			
PS	Example 3; SEQ ID NO 1731; 500pp; English.		
XX			
CC	The invention describes a new isolated polynucleotide (I) encoding a polypeptide with biological activity comprising: a nucleotide sequence of SEQ ID NOS: 1-567 (fully defined); a nucleotide sequence that hybridizes to the sequence of (1) under stringent hybridization conditions; or a nucleotide sequence having greater than 99% sequence identity with the sequence of (1). Also described are: a(n) (expression) vector comprising (I); a host cell genetically engineered to comprise (I) operatively, associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell; an isolated polypeptide comprising a sequence of SEQ ID NOS: 568-1134 (fully defined), where the polypeptide is: a polypeptide encoded by (I); or a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NOS: 1-567; a composition comprising the polypeptide of (3) and a		
RESULT 13			
ADQ96710			
ID	ADQ96710 standard; protein; 466 AA.		
XX			
AC	ADQ96710;		
XX			
DT	23-SEP-2004 (first entry)		
XX			
DE	Human ribonuclease III (RNase III)-like domain.		
XX			
KW	Human; ribonuclease III; RNase III; research purpose; biological purpose;		

KW clinical purpose; cellular interaction.

XX

OS Homo sapiens.

XX US2004126867-A1.

XX PD 01-JUL-2004.

XX PP 09-FEB-2004; 2004US-00774974.

XX PR 06-JUL-2001; 2001US-00900425.

XX (CROO/) CROOKE S T.

PA (WUHH/) WU H.

XX PI Crooke ST, Wu H;

XX DR WPI; 2004-516913/49.

XX PN New isolated nucleic acid molecule encoding human RNase III, useful for

PT research, biological or clinical purposes, e.g. defining the roles of

PT RNase III and the interaction of human RNase III and cellular RNA.

XX PS Example 9, SEQ ID NO 37; 31pp; English.

XX The invention relates to human ribonuclease III (RNase III) and its

CC corresponding nucleic acid sequence. The polynucleotide sequence of the invention is useful for research, biological and clinical purposes. It is useful in defining the roles of RNase III and the interaction of human

CC RNase III and cellular RNA. The present sequence is human RNase III-like

CC domain protein.

XX SQ Sequence 466 AA;

Query Match 32.8%; Score 2463; DB 8; Length 466;  
Best Local Similarity 100.0%; Pred. No. 4e-166; Mismatches 0; Indels 0; Gaps 0;  
Matches 466; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC 909 NPDHARNLSNQNGIROPQKYGDKRKHMMRKEGGINTLNLINIMSRIGQDDPPSPRINERL 968  
1 NPDHARNLSNQNGIROPQKYGDKRKHMMRKEGGINTLNLINIMSRIGQDDPPSPRINERL 60

CC 969 EPLGDAVFLFVSLVHLYLFLPELEGATRATVONQHAMLAKKELDPPMLXAHGP 1028  
61 EPLGDAVFLFVSLVHLYLFLPELEGATRATVONQHAMLAKKELDPPMLXAHGP 120

CC 1029 DICRERDLRHAMNCEREALIGVYLGESLEEKQKOLGRLLNDPDLREWYNTVPPMLQ 1088  
121 DICRERDLRHAMNCFBALIGAVLEGSLSEAKQFGRLLNDPDLREWYNTVPPMLQ 180

Db 1089 QEPNTDQLIETSPVQLOKTEEEAIGVIFVNRLLAFTRTVGENHLTIGHNORMEF 1148  
181 QEPNTDQLIETSPVQLOKTEEEAIGVIFVNRLLAFTRTVGENHLTIGHNORMEF 240

Db 1149 LGDSIMOLVATSYLFLPDRHNEGLTILRASSVNNTQAKAEGMQLMELAINTDKTR 1148  
241 LGDSIMOLVATEYLFLPDRHNEGLTILRASSVNNTQAKAEGMQLMELAINTDKTR 300

Db 1209 PVLGRTKPLADLIESFIAALYDVKDQXVHTMNCVPPRJKEFTFLNQDWDNPKSLQOC 1268  
301 PVLGRTKPLADLIESFIAALYDVKDQXVHTMNCVPPRJKEFTFLNQDWDNPKSLQOC 360

Db 1269 CILTRTEGKEPPILYKLTQTPGSHARTTYTAVYFKGERGCGKGPSIQQEMGAMDA 1328  
361 CILTRTEGKEPPILYKLTQTPGSHARTTYTAVYFKGERGCGKGPSIQQEMGAMDA 420

QY 1329 LEKYNPFQMAHQKRFKGRKQBLKEMWRRHQEREPDETDIKK 1374  
421 LEKYNPFQMAHQKRFKGRKQBLKEMWRRHQEREPDETDIKK 466

ID AAU0587 standard; protein; 378 AA.

XX AAU0587;

XX DT 04-DEC-2001 (first entry)

XX DE Human secreted protein, Seq ID No 579.

XX KW Immunomodulatory; human immunodeficiency virus; HIV; anaemia; angina; rheumatoid arthritis; antiarrhythmic; cardiotonic; vascular; cereoprotective; thrombolytic; antimicrobial; ophthalmological; cytostatic; Alzheimer's disease; Parkinson's disease; human cancer; multiple sclerosis; cancer; hyperproliferative disorder; infection; Gaucher's disease; wound healing.

XX KW thrombosis; wound healing.

XX OS Homo sapiens.

XX PN WO200155326-A2.

XX PD 02-AUG-2001.

XX PR 17-JAN-2001; 2001WO-US001347.

XX PR 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-018874P.

PR 17-MAR-2000; 2000US-019007P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205151P.

PR 20-JUN-2000; 2000US-0205152P.

PR 07-JUL-2000; 2000US-0216647P.

PR 28-JUN-2000; 2000US-0214886P.

PR 07-JUL-2000; 2000US-0215135P.

PR 30-JUN-2000; 2000US-0216880P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-022513P.

PR 14-AUG-2000; 2000US-022514P.

PR 14-AUG-2000; 2000US-022514P.

PR 14-AUG-2000; 2000US-022566P.

PR 14-AUG-2000; 2000US-022566P.

PR 14-AUG-2000; 2000US-022567P.

PR 14-AUG-2000; 2000US-022568P.

PR 14-AUG-2000; 2000US-022568P.

PR 14-AUG-2000; 2000US-022544P.

PR 14-AUG-2000; 2000US-022575P.

PR 14-AUG-2000; 2000US-022575P.

PR 14-AUG-2000; 2000US-022575P.

PR 18-AUG-2000; 2000US-022627P.

PR 22-AUG-2000; 2000US-022668P.

PR 22-AUG-2000; 2000US-0227182P.

PR 23-AUG-2000; 2000US-0227009P.

PR 30-AUG-2000; 2000US-0228924P.

PR 01-SEP-2000; 2000US-022938P.

PR 01-SEP-2000; 2000US-022934P.

PR 01-SEP-2000; 2000US-022945P.

PR 05-SEP-2000; 2000US-0229509P.

PR 05-SEP-2000; 2000US-0229513P.

PR 06-SEP-2000; 2000US-023043P.

PR 08-SEP-2000; 2000US-0230438P.

PR 08-SEP-2000; 2000US-0231243P.

PR 08-SEP-2000; 2000US-0231244P.

PR 08-SEP-2000; 2000US-0231414P.

RESULT 14

,AAU20587

PR 08-SEP-2000; 2000US-0232080P.  
 PR 08-SEP-2000; 2000US-0232081P.  
 PR 12-SEP-2000; 2000US-0231968P.  
 PR 14-SEP-2000; 2000US-0232397P.  
 PR 14-SEP-2000; 2000US-0232398P.  
 PR 14-SEP-2000; 2000US-0232399P.  
 PR 14-SEP-2000; 2000US-0232400P.  
 PR 14-SEP-2000; 2000US-0232401P.  
 PR 14-SEP-2000; 2000US-0233063P.  
 PR 14-SEP-2000; 2000US-0233064P.  
 PR 14-SEP-2000; 2000US-0233065P.  
 PR 21-SEP-2000; 2000US-0234223P.  
 PR 21-SEP-2000; 2000US-0234274P.  
 PR 25-SEP-2000; 2000US-0234398P.  
 PR 26-SEP-2000; 2000US-0235349P.  
 PR 27-SEP-2000; 2000US-0235354P.  
 PR 29-SEP-2000; 2000US-0236369P.  
 PR 29-SEP-2000; 2000US-0236370P.  
 PR 02-OCT-2000; 2000US-0236302P.  
 PR 02-OCT-2000; 2000US-0237037P.  
 PR 02-OCT-2000; 2000US-0237038P.  
 PR 02-OCT-2000; 2000US-0237039P.  
 PR 13-OCT-2000; 2000US-0239935P.  
 PR 13-OCT-2000; 2000US-0239937P.  
 PR 20-OCT-2000; 2000US-024060P.  
 PR 20-OCT-2000; 2000US-0241221P.  
 PR 20-OCT-2000; 2000US-0241785P.  
 PR 20-OCT-2000; 2000US-0241786P.  
 PR 20-OCT-2000; 2000US-024187P.  
 PR 20-OCT-2000; 2000US-0241908P.  
 PR 20-OCT-2000; 2000US-0241909P.  
 PR 01-NOV-2000; 2000US-0241926P.  
 PR 08-NOV-2000; 2000US-0244617P.  
 PR 08-NOV-2000; 2000US-024674P.  
 PR 08-NOV-2000; 2000US-024675P.  
 PR 08-NOV-2000; 2000US-024676P.  
 PR 08-NOV-2000; 2000US-024677P.  
 PR 08-NOV-2000; 2000US-024678P.  
 PR 08-NOV-2000; 2000US-0246785P.  
 PR 08-NOV-2000; 2000US-0246524P.  
 PR 08-NOV-2000; 2000US-0246525P.  
 PR 08-NOV-2000; 2000US-0246526P.  
 PR 08-NOV-2000; 2000US-0246527P.  
 PR 08-NOV-2000; 2000US-0246528P.  
 PR 08-NOV-2000; 2000US-0246532P.  
 PR 08-NOV-2000; 2000US-0246509P.  
 PR 08-NOV-2000; 2000US-0246510P.  
 PR 08-NOV-2000; 2000US-0246611P.  
 PR 17-NOV-2000; 2000US-0246613P.  
 PR 17-NOV-2000; 2000US-0249207P.  
 PR 17-NOV-2000; 2000US-0249308P.  
 PR 17-NOV-2000; 2000US-0249309P.  
 PR 17-NOV-2000; 2000US-0249310P.  
 PR 17-NOV-2000; 2000US-0249321P.  
 PR 17-NOV-2000; 2000US-0249212P.  
 PR 17-NOV-2000; 2000US-0249213P.  
 PR 17-NOV-2000; 2000US-0249214P.  
 PR 17-NOV-2000; 2000US-0249215P.  
 PR 17-NOV-2000; 2000US-0249216P.  
 PR 17-NOV-2000; 2000US-0249217P.  
 PR 17-NOV-2000; 2000US-0249218P.  
 PR 17-NOV-2000; 2000US-0249344P.  
 PR 17-NOV-2000; 2000US-0249245P.  
 PR 17-NOV-2000; 2000US-0249364P.  
 PR 17-NOV-2000; 2000US-0249365P.  
 PR 17-NOV-2000; 2000US-0249397P.  
 PR 17-NOV-2000; 2000US-0249399P.

PR 08-SEP-2000; 2000US-0249300P.  
 PR 01-DEC-2000; 2000US-0250160P.  
 PR 01-DEC-2000; 2000US-0250191P.  
 PR 05-DEC-2000; 2000US-0250300P.  
 PR 05-DEC-2000; 2000US-0250309P.  
 PR 08-DEC-2000; 2000US-0251989P.  
 PR 08-DEC-2000; 2000US-0251990P.  
 PR 11-DEC-2000; 2000US-0254097P.  
 PR 05-JAN-2001; 2001US-0259678P.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Barash SC, Ruben SM,  
 DR XX  
 DR N-PSDB; AAS33296.  
 XX  
 PT New nucleic acids and polypeptides, useful for diagnosing, preventing or  
 PT treating medical conditions.  
 XX  
 PS  
 XX  
 CC The invention relates to novel isolated nucleic acid molecules (I).  
 CC encoding human secreted proteins (II). (I) and (II) are used to prevent,  
 CC treat or ameliorate a medical condition in e.g. humans, mice, rabbits,  
 CC goats, horses, cats, dogs, chickens or sheep. (I) and (II) may be used in  
 CC the prevention, treatment and diagnosis of diseases associated with  
 CC inappropriate expression of secreted proteins. (I) and complementary  
 CC sequences may also be used as DNA probes in diagnostic assays (e.g.  
 CC polymerase chain reactions (PCR) to detect and quantify the presence  
 CC of similar nucleic acid sequences in samples, and so which patients may  
 CC be in need of restorative therapy. (II) may also be used as antigens in  
 CC the production of antibodies and in assays to identify modulators  
 CC (agonists and antagonists) of the expression and activity of the secreted  
 CC proteins. The anti-(II) antibodies and antagonists may also be used to  
 CC down regulate expression and activity of (II). The anti-(II) antibodies  
 CC may also be used as diagnostic agents for detecting the presence of (II)  
 CC in samples (e.g. by enzyme linked immunosorbent assay (ELISA)). The  
 CC disorders include for example: immune/autoimmune diseases (e.g. HIV  
 CC (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis  
 CC and multiple Sclerosis), cancers and hyperproliferative disorders (e.g.  
 CC melanomas, neoplasms of the breast or liver, Sezary syndrome and  
 CC Gaucher's disease), neurological diseases (e.g. Alzheimer's disease,  
 CC Parkinson's disease and Charcot-Marie-Tooth disease), cardio-/  
 CC cerebrovascular disorders (e.g. cardiac arrest, tachyarrhythmia, angina and  
 CC thrombosis), infections caused by bacteria, viruses and fungi and ocular  
 CC disorders (e.g. corneal infections). (I) and (II), agonists, antagonists  
 CC and antibodies can also be used to promote wound healing, maintain organs  
 CC before transplantation, and support cell culture of primary tissues.

Query Match 26.1%; Score 1961; DB 4; Length 378;  
 Best Local Similarity 98.9%; Pred. No. 1.4e-130; Indels 0; Gaps 0;  
 Matches 374; Conservative 0; Mismatches 4;

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 1 ATYRTAIIVQNHQHMLAKKLELDPEMLYAHQHDPLCRESDLRHAMANCFEALIGAVLGS 60  
 Db 1057 LBEAKOLFGRLLFDREYWLNYPHLPLQLOEPNTDROLJETSPVLUQLTTEFRAIGV 1116  
 61 LBEAKOLFGRLLFDREYWLNYPHLPLQLOEPNTDROLJETSPVLUQLTTEFRAIGV 120  
 Db 1117 IPTHVRLARAFTRTGFHMLTGHQRMFLGLGSIMQVATEYLFIHPPDHHECHTL 1176  
 Db 121 IPTHVRLARAFTRTGFHMLTGHQRMFLGLGSIMQVATEYLFIHPPDHHECHTL 180  
 Qy 1171 LRSLVANNRTOQVAEELGMQBEYAITNDKTRPGVGRKTILADLIESFIAUYTDKDLY 1236

RESULT 15

AAU21744

ID AAU21744 standard; protein; 378 AA.

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AC

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AAU21744;

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DT 04-DEC-2001. (first entry)

XX

DE Novel human neoplastic disease associated polypeptide #177.

XX

KW Human; neoplastic disease associated polypeptide; cancer; hyperproliferative disorder; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; renal disorder; neuroprotective; cytopstatic; anti inflammatory; vasotropic.

XX

OS Homo sapiens.

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PN WO200155163-A1.

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PD 02-AUG-2001.

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PR 17-JAN-2001; 2001WO-US001358.

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PR 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180028P.

PR 24-FEB-2000; 2000US-0184564P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189074P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214986P.

PR 07-JUL-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-021680P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225213P.

PR 14-AUG-2000; 2000US-0225214P.

PR 14-AUG-2000; 2000US-0225263P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-022568P.

PR 14-AUG-2000; 2000US-022570P.

PR 14-AUG-2000; 2000US-022571P.

PR 14-AUG-2000; 2000US-0225757P.

PR 14-AUG-2000; 2000US-0225758P.

PR 14-AUG-2000; 2000US-0225759P.

PR 18-AUG-2000; 2000US-0226219P.

PR 22-AUG-2000; 2000US-0226681P.

PR 22-AUG-2000; 2000US-022688P.

PR 22-AUG-2000; 2000US-0227182P.

PR 23-AUG-2000; 2000US-0227009P.

PR 01-SEP-2000; 2000US-0228924P.

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PR 01-SEP-2000; 2000US-0229343P.

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PR 06-SEP-2000; 2000US-0230438P.

PR 08-SEP-2000; 2000US-0231242P.

PR 08-SEP-2000; 2000US-0231243P.

PR 08-SEP-2000; 2000US-0231244P.

PR 08-SEP-2000; 2000US-0231414P.

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PR 08-SEP-2000; 2000US-0233080P.

PR 12-SEP-2000; 2000US-0233140P.

PR 14-SEP-2000; 2000US-0233141P.

PR 14-SEP-2000; 2000US-0233299P.

PR 14-SEP-2000; 2000US-0233400P.

PR 14-SEP-2000; 2000US-023363P.

PR 14-SEP-2000; 2000US-023364P.

PR 14-SEP-2000; 2000US-023365P.

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PR 21-SEP-2000; 2000US-0244274P.

PR 25-SEP-2000; 2000US-0244997P.

PR 26-SEP-2000; 2000US-0235834P.

PR 27-SEP-2000; 2000US-0235836P.

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PR 29-SEP-2000; 2000US-0235367P.

PR 29-SEP-2000; 2000US-0236368P.

PR 29-SEP-2000; 2000US-0236369P.

PR 02-OCT-2000; 2000US-0236802P.

PR 02-OCT-2000; 2000US-0237037P.

PR 02-OCT-2000; 2000US-0237038P.

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PR 20-OCT-2000; 2000US-0240860P.

PR 20-OCT-2000; 2000US-0241221P.

PR 20-OCT-2000; 2000US-0241785P.

PR 20-OCT-2000; 2000US-0241786P.

PR 20-OCT-2000; 2000US-0241808P.

PR 20-OCT-2000; 2000US-0241809P.

PR 01-NOV-2000; 2000US-0244617P.

PR 08-NOV-2000; 2000US-0246474P.

PR 08-NOV-2000; 2000US-0246475P.

PR 08-NOV-2000; 2000US-0246476P.

PR 08-NOV-2000; 2000US-0246477P.

PR 08-NOV-2000; 2000US-0246478P.

PR 08-NOV-2000; 2000US-0246532P.

PR 08-NOV-2000; 2000US-0246533P.

PR 08-NOV-2000; 2000US-0246609P.

PR 08-NOV-2000; 2000US-0246610P.

PR 08-NOV-2000; 2000US-0246611P.

PR 08-NOV-2000; 2000US-0246613P.

PR 17-NOV-2000; 2000US-0249007P.

PR 17-NOV-2000; 2000US-0249209P.

PR 17-NOV-2000; 2000US-2249210P.  
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 PR 17-NOV-2000; 2000US-2249212P.  
 PR 17-NOV-2000; 2000US-2249213P.  
 PR 17-NOV-2000; 2000US-2249214P.  
 PR 17-NOV-2000; 2000US-0249215P.  
 PR 17-NOV-2000; 2000US-0249216P.  
 PR 17-NOV-2000; 2000US-0249217P.  
 PR 17-NOV-2000; 2000US-0249218P.  
 PR 17-NOV-2000; 2000US-0249244P.  
 PR 17-NOV-2000; 2000US-0249245P.  
 PR 17-NOV-2000; 2000US-0249264P.  
 PR 17-NOV-2000; 2000US-0249265P.  
 PR 17-NOV-2000; 2000US-0249277P.  
 PR 17-NOV-2000; 2000US-0249299P.  
 PR 17-NOV-2000; 2000US-0249300P.  
 PR 01-DEC-2000; 2000US-0250160P.  
 PR 01-DEC-2000; 2000US-0250191P.  
 PR 05-DEC-2000; 2000US-0251030P.  
 PR 05-DEC-2000; 2000US-0251988P.  
 PR 05-DEC-2000; 2000US-0251989P.  
 PR 06-DEC-2000; 2000US-025179P.  
 PR 08-DEC-2000; 2000US-0251856P.  
 PR 08-DEC-2000; 2000US-0251868P.  
 PR 08-DEC-2000; 2000US-0251869P.  
 PR 08-DEC-2000; 2000US-0251989P.  
 PR 08-DEC-2000; 2000US-0251990P.  
 PR 11-DEC-2000; 2000US-0254097P.  
 PR 05-JAN-2001; 2001US-0259678P.  
 XX  
 PA (HUMA-) HUMAN GBNOMB SCI INC.  
 XX  
 PI Rosen CA, Barash SC, Ruben SM;  
 XX  
 DR N-PSDB; AU334943.  
 XX  
 PT Novel polypeptides and poly nucleotides useful as diagnostic reagents to  
 PT diagnose diseases or disorders associated with aberrant expression or  
 PT activity of polypeptides, and for treating cancers, rheumatoid arthritis.  
 XX  
 PS Claim 11; SEQ ID NO 471; 687pp; English.

CC The present invention relates to the isolation of novel human neoplastic  
 CC disease associated polypeptides, and cDNA (AU334767-AU335050) and DNA  
 CC sequences encoding for these polypeptides. The sequences of the invention  
 CC are useful in the diagnosis, treatment, prevention and/or prognosis of  
 CC disorders involving neoplastic disease such as hyperproliferative  
 CC disorders (e.g. leukemia, bone cancer, bladder cancer, brain stem  
 CC glioma, adult liver cancer, childhood cerebellar astrocytoma, or  
 CC Hodgkin's lymphoma). The sequences of the invention may also be useful  
 CC for treating other disorders such as neural disorders, immune system  
 CC disorders, muscular disorders, reproductive disorders, gastrointestinal  
 CC disorders, pulmonary disorders, cardiovascular disorders and renal  
 CC disorders. The polynucleotide sequences of the invention are also useful  
 CC in gene therapy. AU331568-AU321851 represent the novel human neoplastic  
 CC disease associated polypeptides of the invention. Note: The sequence data  
 CC for this patent did not form part of the printed specification, but was  
 CC obtained in electronic format directly from WIPO at  
 CC [ftp://wipo.int/pub/published\\_pct\\_sequences](ftp://wipo.int/pub/published_pct_sequences)  
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 Sequence 378 AA;

Query Match 26.1%; Score 1961; DB 4; Length 378;

Best Local Similarity 98.9%; Pct. No. 1 4e-130; Mismatches 4; Indels 0; Gaps 0;  
 Matches 374; Conservative 1

Qy 997 ATYRTAIVQNLMLAKKLEDPPFLYAHGDLICRSDRLRMANCPEALIGAVLEG 1056  
 Db 1 ATYRTAIVQNLMLAKKLEDPPFLYAHGDLICRSDRLRMANCPEALIGAVLEG 60  
 Qy 1057 LEEAKQQLFGRLLFNDPDLREVLNLYPLHPLQIQPNTDRQLLETSPVLUQKLTTEFEAIGV 1116

Search completed: February 3, 2006, 19:36:16  
 Job time : 219 secs

Db 61 LEEAKQQLFGRLLFNDPDLREVLNLYPLHPLQIQPNTDRQLLETSPVLUQKLTTEFEAIGV 120  
 Qy 1117 ITPHVRLLARATFLRTVGFNHLITLGHNQRMFLGDSIMQLQVATEYIFHFFPDHHEGLTL 1176  
 Db 121 ITPHVRLLARATFLRTVGFNHLITLGHNQRMFLGDSIMQLQVATEYIFHFFPDHHEGLTL 180  
 Qy 1117 LRSLSLVRNRTQAKVASELGMQMYAITNDKTRPVQGRTKTLADLUSPFIALLYTDKLEY 1236  
 Db 181 LRSLSLVRNRTQAKVASELGMQMYAITNDKTRPVQALRTKTLADLUSPFIALLYTDKLEY 240  
 Qy 1237 VHTPMNCCFPKLFELINQDNDPKSQLQCCLTURTEGKEDPDIPLYKLTQTVGSHAR 1296  
 Db 241 VHTPMNCCFPKLFELINQDNDPKSQLQCCLTURTEGKEDPDIPLYKLTQTVGSHAR 300  
 Qy 1297 TYTVAVYFGERITGCGKGPKSIQQAEMGAMDALEKYNFPOMAHQKRTGKRYQELKMR 1356  
 Db 301 TYTVAVYFGERIGCGKGPKSIQQAEMGAMDALEKYNFPOMAHQKRTGKRYQELKMR 360  
 Qy 1357 WREHQEREPDTEICK 1374  
 Db 361 WREHQEREPDTEICK 378

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GenCore version 5.1.7  
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Om protein - protein search, using Bw model

Run on: February 3, 2006, 19:36:34 ; Search time 55 Seconds

(without alignments)  
2403.670 Million cell updates/sec

Title: Perfect score: US-10-079-185-2  
Sequence: 1 MMQANTCHMSFHPRGRGPR.....MRWEREHQREPDETDKK 1374

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96316763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
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Listing First 45 summaries

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Db	176 IEDYDILGETPAHNAKAFDAQIVIVNGQVLGKGSQRTKKQABQSAQFAIN---OLTHR 229	RESULT 7
C;Species: Mus musculus (house mouse)	proliferation potential-related protein - mouse	
C;Date: 11-Jan-2000	#sequence_revision 11-Jan-2000	#text_change 09-Jul-2004
C;Accession: T4227		
R;Witte, M.M.; Scott, R.E.		
A;Reference number: 22246	submitted to the EMBL Data Library, November 1998	
A;Accession: T4227		
A;Status: preliminary; translated from GB/EMBL/DBJ		
A;Molecule type: mRNA		
A;Residues: 1-1560 <WIT>		
A;Cross-references: UNIPROT:P97868; UNIPARC:UPI000028767; EMBL:U83913; NID:93858884; P1		
A;Experimental source: strain Balb/C		
A;Genetics: P2P-R		
C;Function: A;Description: involved in hnRNP association and Rb1 binding		
P;57-107/Domain: RING finger homology <RRN>		
Query Match 3.9%; Score 293; DB 2; Length 1560; Best Local Similarity 23.8%; Pred. No. 1; 3e-07; Matches 151; Conservative 72; Mismatches 200; Indels 212; Gaps 34; Qy 25 HGARPSA-PSFRPQURLHQQPQPVQYQEPSSA-----PSTIFSNSPANFLP 73 Db 296 NARPGGGRPGWBSN-KLGYIVLSPQOIRRGRSCYRSINGRHRSERSORTQGSPS-LP 353 Qy 74 PRPDFVPPPPNPPNSAQAGLPLPPCPIRPPPNQMRHPPVPPCFPPMPPMCPNPPNPPV 133 Db 354 ATPVFPVFPVPP-----PLVPPPP-----HTLPLP-----PGVLPQGPQGP-----P 391 Qy 134 GRPPGCTTPEPFRMPPMPPMPP-----PPPPMOCQVNT----- 166 Db 392 GQPPTAG--VSVPVPPGPAPPANISTACFSPGVPTAHNTMPTQAPLSSREEFYREQ 448 Qy 167 -----QYP-----PGYSHNFPFSPMSFNSQNFNPPSSFIPSANNSSSPFHRHPPYPLPKAPS 217 Db 449 RIKEESKFPYSSGSSYRSYSSYTDKSRSRGSSTRSRSYRSFSRSHRSRSYSSRPPY----- 502 Qy 218 ERSPERLKHDDHARDHSGRGERHSRDRERGRSPDARRQDSRYSRSDY-RQRTPS 276 Db 503 -RGRGKSKRSN--RCSRSHG--YHRS----RSRSPYRHSRSRSPQAFQSQPT 550 Qy 277 RRSYERSRERER-HRR-----DRSPSPLRSRSYKEYR 313 Db 551 K-RNVRPG-EERERYFNRREVPPPDYKAVYGRSVDPRDFPEKERYREWERKRYREWKR 608 Qy 314 SGRSGLSSVWPERPAGCPELSEILOKTDWAP----PLEVUNHSPSRECKRAMWEEK 369 Db 609 YYKGYAVGAQPRPSA-----NREDFSPERLPLNIRN--SPPTGRGREDYAQG 655 Qy 370 DRWSDN-----QSSGDKNTISIKEKEPEITMD-----KNE--EE 403 Db 656 SHRNRRNUGGGNPEKLSRDRSHNAKDKNSKSKERSENVPGDKEKGKHKHRKRGRNBERGE 715 Qy 404 EEEELKRVWV-----RCHSENY-----YSSDMQDVQDSTVVGTSR 440 Db 716 SESFLNPELGLGKFRKCRGSSGIDETKDTLFVPPRSRDRATVURDFMD--AESITPKSV 773 Qy 441 LRDLYKPFEEEGSRSQKAKA-----ARPPPEPKKULDELESSSESE---CES 487 Db 774 DDKREKDKPKVSKDKTGRKSOGSATAKKDNVTLKPSKGQEKVGDGDRKEKSPRSEPLKA 833 Qy 488 DE DST-----CSSSDSEFVFDVIAKIKKKH 514 Db 834 KEATKLDVKSSQSSQDEKVKTGT----PRKAH 863	RESULT 8	
B82073	ribonuclease III VC2461 [imported] - <i>Vibrio cholerae</i> (strain N16961 serogroup O1)	
C;Species: <i>Vibrio cholerae</i>		
C;Date: 18-Aug-2000	#sequence_revision 20-Aug-2000	#text_change 09-Jul-2004
C;Accession: B82073		
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;		
Charlson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.		
I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.		
Nature 406, 477-483, 2000		
A;Title: DNA sequence of both chromosomes of the cholera pathogen <i>Vibrio cholerae</i> .		
A;Reference number: A82035; MUID:2046533; PMID:10952101		
A;Accession: B82073		
A;Status: preliminary		
A;Molecule type: DNA		
A;Residues: 1-225 <HEI>		
A;Cross-references: UNIPROT:O9KPB2; UNIPARC:UPI000114369; GB:AE004316; GB:AE003852; NID: P1		
A;Experimental source: Serogroup O1; strain N16961; biotype El Tor		
A;Genetics: C;Genetics: C;Function: C;Superfamily: ribonuclease III; double-stranded RNA-binding repeat homology		
P;1		
Query Match 3.8%; Score 285; DB 2; Length 225; Best Local Similarity 32.2%; Pred. No. 2.8e-08; Matches 75; Conservative 42; Mismatches 101; Indels 15; Gaps 5; Qy 1101 SPVLOKUTEFEEAIGVIFTHRLRLLAFTLRTVGFNHLTGHNORMBFLGDSIMOLVATE 1160 Db 2 TPPMNLKT--SKLGYTFKTELLNLALIHTHSANGK---HNERLEFFGDSLSFVIA 53 Qy 1161 YLFINHEPDHNGEHLTILRSILVNNRTOAKYABEGLMNOEYAIITNDKTKRPGVLRKTK-LAD 1219 Db 54 ELYRRFPKVNEGDMSRMRAITLVRGNTLAEELGREFDGLDYLKLGPGELKSGGFRRD SILAD 113 Qy 1220 LLESFIALLAIVTDKOLEYVWHTMANVCFPRJKEFILQDWDWPKSOLQCCULTRREGKEP 1279 Db 114 AVEAIIQAYLDSLTDATRSIYLVENYHGRLEBIEKPGASQDKPTRLQF---LQGRK 168 Qy 1280 DIPLYKTLQVGPASHARTYVAVYFKG-ERIGCKGKPSIQCQEMGAMDALEK 1331 Db 169 PLPVYVWTNKGAEHNQEFVACEYAGMDPVPVIGKTSRKIAQAAETALEQ 221	RESULT 9	
AB3961	ribonuclease III rncS [imported] - <i>Bacillus halodurans</i> (strain C-125)	
C;Species: <i>Bacillus halodurans</i>		
C;Date: 01-Dec-2000	#sequence_revision 01-Dec-2000	#text_change 09-Jul-2004
C;Accession: AB3961		
R;Tatami, H.; Nakatome, K.; Takak, Y.; Maeno, G.; Saaki, R.; Masui, N.; Fuji, F.; Hiran		
Nucleic Acids Res. 28, 4317-4331, 2000		
A;Title: Complete genome sequence of the alkaliophilic bacterium <i>Bacillus halodurans</i> and its relationship to <i>Bacillus subtilis</i>		
A;Reference number: AB3650; MUID:2051282; PMID:11058132		
A;Accession: AB3961		
A;Status: preliminary		
A;Molecule type: DNA		
A;Residues: 1-263 <STO>		
A;Cross-references: UNIPROT:O9KA05; UNIPARC:UPI000134340; GB:AP001515; GB:BA000004; NID: P1		
C;Genetics: C;Superfamily: ribonuclease III; double-stranded RNA-binding repeat homology		
Query Match 3.8%; Score 282; DB 2; Length 263; Best Local Similarity 30.9%; Pred. No. 5.2e-08; Matches 77; Conservative 50; Mismatches 110; Indels 12; Gaps 5; Qy 1084 HPLQLOEPNTDQRLQETSPVLOKUTEFEEAIGVIFTHRLRLLAFTLRTVGFNHLTGHNORMBFLGDSIMOLVATE 1141 Db 15 HSERRQ---KRLTLLTAKQOMDPBLRTNLTFANKKLUVOAFTHSYNEHRTQSK 71 Qy 1142 HNORMEFLGLSIMOLVATEVLFHFDHNGEHLTILRSILVNNRTOAKVABEGLMNOEYAI 1201		

Db	72 DNERCERFLGDAVLEAVSQVILYKAFQEMSEGDMDKRASTIVCEPSAQLABELHFSBLV 131	
Qy	1202 TNDKTKRPPVG-LRTKTLADLIESFIAALYTKDEYVHTFMNVCPPRKLKEPLNQDWD 1260	
Db	132 LGKGSEMTGGRKRPALLADVFESFVGALYDQGMDAVYFLBERTYPKISBGAFH-MMD 190	
Qy	1261 PRSQQQCCLTRTESEKEPDIPLKYLQTVGSHARTYTVAVYKPERIGKGPIQQA 1320	
Db	191 FKSQDQEF---IQDRNLGHIVYEVQERGAHNRKFVSEVNLNBTLGVTGRSKKEA 245	
Qy	1321 EMGAAMDAL 1329	
Db	246 EOHAQOAL 254	
RESULT 10		
F98012	ribonuclease III (EC 3.1.26.3) [imported] - <i>Streptococcus pneumoniae</i> (strain R6)	
C;Species:	<i>Streptococcus pneumoniae</i>	
C;Date:	22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004	
C;Accession:	F98012	
R;Bioskins, J.A.; Aborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; Dehoff, B.S.; E; R.; LeBlanc, J.A.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M; Y.; P.; Sun, P.M.; Winkles, M.E.		
J. Bacteriol. 183, 5709-5717, 2001		
A;Authors:	Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A;Title:	Genome of the Bacterium <i>Streptococcus pneumoniae</i> Strain R6.
A;Reference number:	A97872; MUID:21429245; PMID:1544234	
A;Status:	preliminary	
A;Molecule type:	DNA	
A;Residues:	1-232 <KUR>	
A;Cross-references:	UNIPROT:Q8DPJ8; UNIPARC:UPI0000E35D9; GB:AE007317; PIDN:AAK99930.1;	
C;Genetics:		
C;Gene:	rncS	
C;Superfamily:	ribonuclease III; double-stranded RNA-binding repeat homology	
Query Match	3.8%; Score 281.5; DB 2; Length 232;	
Best Local Similarity	32.9%; Pred. No. 4.7e-08;	
Matches	79; Conservative 47; Mismatches 91; Indels 23; Gaps 9;	
Qy	1099 ETSPVYQKLTFEEAIGVIFHVRLLARAFTIRTGENH-LTIGHNQRMFLGDSIMQL 1156	
Db	3 BLQTVLKHFFIE---FADKKLLETAFTHTSYANEHRLKISNERLPLGDAVQL 56	
Qy	1157 VATEYLIFHEDPHCHTLTSSLNUNRTOVKARVABLGMOBYATNDKTKRPPGARTK- 1215	
Db	57 LISEMVYKVKRKEPGDLSKURAMITREESLAGFADQCFQDFP-TIKGKGEBKGGNRD 115	
Qy	1216 -TLDLLESFIAALYTKDQLEYVHTFMNVCPPRKL-EFLINQMDPQSQLOQCLTL 1272	
Db	116 TILGAFEAFGLALIDKDVAKVYKEFYIQWMPKVGAEFEMITY--KTHLQE--LL 169	
Qy	1273 RTEGKBDPDIPL-YKTMQTVGSHARTYTVAVYKGERIGCGKGPSIQAENGAMDALEK 1331	
Db	170 QVNG---DVAIRQVQISETGPADKVFDFEVILVEKGSIGOGGRSKKLAEOERAKNAVEK 226	
RESULT 11		
H95344	ribonuclease III [imported] - <i>Streptococcus pneumoniae</i> (strain TIGR4)	
C;Species:	<i>Streptococcus pneumoniae</i>	
C;Date:	03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004	
C;Accession:	H95144	
R;Nettles, H.; Nelson, K.E.; Paulsen, I.T.; Bisen, J.A.; Read, T.D.; Peterson, S.; Heidorn, J.D.; Umeyama, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, T.; Hickey, E.K.; Holt, I.E.		
Science 293, 498-506, 2001		
A;Authors:	Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title:	Complete Genome Sequence of a virulent isolate of <i>Streptococcus pneumoniae</i> .
A;Reference number:	A95000; MUID:21357209; PMID:11463916	
A;Accession:	H95144	
Qy	171 -----GYSHHNPPPSNS 184	
Db	378 PVFVPPVPP-----PLVPPPP-----HTLPLP--PGVPPQFSQPFP--IQQ 415	
Qy	136 PRQGQTFEFMMPRPSMHPPPRPPRPMQDYN-----YQYPP----- 170	
Db	416 PPRAG---YSPPPGFP-PAPANLSTPWAQPSGQTAHNTIPTQAPPSSREEFYRQR 471	
Qy	76 PDRFVPPPPMPPSAQGPLPPCPTRPFPNHQMHPFPVPPCFPPMPPMPCPNPPVPG 135	
Db	320 ARGGGGGGWEN-KGQYLVSSPQQTGRGRCSYRSINRGRHRSRSRQTQPS-LPAT 377	
Qy	171 -----GYSHHNPPPSNS 184	
Db	472 LKEEEKKSKLDDEFTNDPAKELMEYKKIQRERRRSRSKSPYSGSSYSSRTYSKRS 531	
Qy	185 FQNPNSFLPSANNSSSHFRHLPPYLPKAPSERRSRPLKHYDDHRRDHGRGRPH 244	



QY 1039 -AMANCFEALIIGAVVLEGLSBEAKLQFLGRFLFN--DPDLREWMVYPLHPLQLOBPNTD 1094  
 Db 1090 KSVSDCAEALIJGAYVGGGLSASLIMMKWLGDVDFDPLVWETANRV--SLRCVTPKED 1147  
 QY 1095 RQLIETSPVQKUJFREEAIGVIFTVRLARAFTRTGVFENHLTQH--QRMPLGD 1151  
 Db 1148 -----ELTELERKIQHEFFAKLKEAT-----HSLRESYYERAFRLGD 1189  
 QY 1152 SIMQVQATEYLFIHPPDHHEGHLTURSSLYNRTQAKVAB-----ELGM 1195  
 Db 1190 SVLDFLITRHLFNTYEQTGFCGEMTDLRSACUNNERFAQAVKNNLTHLQRCAUTLSTQI 1249  
 QY 1197 QEVAT--NDKTR--PVGURTKTLADLIESFLIALYTDKLEYVHTEMKNCFPRLK 1251  
 Db 1250 NDYLNFSOKPDETGSRISPIQKALGQDVYESTAGALLIDTRDQDWR--VFPBLSP 1307  
 QY 1252 FILMDQWN-DPKSQIQQCCUTL---RTEGKEDPDIYKIQ-----TVGSPHARTY 1299  
 Db 1308 LVTPKLQLPYRENLNLSGLYFPRVKNSNDGKQATQLOQDQDVLJTGDSBQ-- 1365  
 QY 1300 VAVYFKGERIGCGKRSIQQEMGAANDALEKYNFPOMAKRFGRKY---RQBLKEM 1355  
 Db 1366 -----NKALGKASHLTLT-----EKRNSRKTSIGDNQSSMDV 1401  
 QY 1356 RWEREHQER--PDTEDIK 1373  
 Db 1402 NLACNHSDRDTLTSBTTEIO 1421

RESULT 15

hypothetical protein FHR2.17 [imported] - *Arabidopsis thaliana* (mouse-ear cress)

C-Species: *Arabidopsis thaliana* (mouse-ear cress)

C-Accession: G86292

R-Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conin, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Hansen, B.; Huizar, L.; Nature 408, 816-820, 2000

A-Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hobson, C.; Khan, S.; Khaykin, E.; Kim, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luroe, J.S.; Maiti, R.; Marziali, A.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, M.; Wu, D.; Yu, J.; Frazer, C.M.; Venter, J.C.; Davis, R.W.

A-Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.

A-Reference number: A86141; PMID:21016719; PMID:1130712

A-Accession: G86292

A-Status: preliminary

A-Molecule type: DNA

A-Residues: 1-1005 <STO>

A-Cross-references: UNIPROT:Q9LMQ1; UNIPARC:UPI00000A2407; GB:AE005172; NID:98927662; PI: C; Genetics; A; Map position: 1

Query Match 3 64%; Score 273.5; DB 2; Length 1006;

Best Local Similarity 32.9%; Pred No. 8e-07; Mismatches 99; Conservative 17; Indels 87; Gaps 19;

Matches 99; Conservative 17; Mismatches 98; Indels 87; Gaps 19;

QY 3 QGNTCHRMSSHPGRCGCPRGK-----GHCARPSAASFRPQNLRLHQQP 47  
 Db 4B QSNRGRRS-----GSSRNRRSSCDPQYQFLDTCGHWRPTTSS--PENPFL--PFPQ 98  
 QY 4B PVQKYEPSSAPSTTFNSNAPNFIPRPRDFVW-FPPPMPSAQQGQLPPCPIRPPPNHQ 106  
 Db 99 P-----RPPPRR-----PRPRSPRIPRPLVSPPPPLHPRP--SFCPPPL 138  
 QY 107 MRHPRPVUPCPFPMPMPCCNNPPVPGAPRQGTFP-----FLKMPPPRSPHPPPPPM 160  
 Db 139 MPSPLVPS-PPPPPLVPSLVPSP-----PPSPPPFFFFPSPPPPVTFPPPLVSPSPPLPG 196  
 QY 161 PQQIVWQVQPGYSHNFPPLSPNSQNPSPLSANSSSPHFLHPP--YPLPKAPS 217

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## **Protein Sequence Searches - February 2005**

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

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GenCore version 5.1.7  
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Om protein - protein search, using sw model

Run on: February 3, 2006, 19:32:44 ; Search time 287 Seconds  
 (without alignments)  
 3377.686 Million cell updates/sec

Title: Perfect score: US-10-079-185-2

Sequence: 7500

1 MMQANTCHRMSSFFPGRCPR..... MMRWREHOREPDETEDKK 1374

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

216643 seqs, 705523306 residues

Total number of hits satisfying chosen parameters: 216643

Minimum DB seq length: 0  
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing First 45 summaries

Database : UniProt 05.80.\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	7471	99.6	1374	RNC_HUMAN
2	7160	95.5	1373	Oshzj0_MOUSE
3	6380	85.1	1231	Ospaj6_MOUSE
4	6344.5	84.6	1336	Oszir3_CHICK
5	5217	69.6	1021	Osp269_MOUSE
6	4982	66.4	942	Ospf88_MOUSE
7	4121	54.9	780	Otmib_MOUSE
8	3767	50.2	1041	Oskwl_tetradon
9	3696	49.3	20705	Osbj0_MOUSE
10	2963	39.5	1327	Oxkyns_DROME
11	2881.5	38.4	979	Ostok8_ANOGA
12	2825	37.7	541	Ostqk8_ANOGA
13	2811.5	37.5	1071	Osp04_DROME
14	1683.5	35.8	836	Otpneb_ANOGA
15	2298	30.6	432	Osp005_MOUSE
16	1480	19.7	2288	Osp698_RAT
17	1473.5	19.6	1061	O61xx9_CAEEL
18	1448	19.3	1086	RNC_CAEEL
19	1154.5	29.0	2	O48Kw3_DROME
20	1138.5	15.2	412	O569m4_XENLA
21	711	9.5	134	O569g2_MOUSE
22	344.5	4.6	230	O82g2l_ENTFA
23	340.5	4.5	1150	O81mm6_DROME
24	340	4.5	846	O8mrp6_DROME
25	340	4.5	1109	Ogvav4_DROME
26	339	4.5	1389	O55f61_DICDD
27	331	4.4	1838	O6bcj9_TETTH
28	329.5	4.4	2869	O60pd2_CAEEL
29	328	4.4	1022	O48px9_TETNG
30	328	4.3	551	O8Bx18_MOUSE
31	321	2	249	O65j95_BACLD

### ALIGNMENTS

32	321	4.3	551	2	Q8X86_MOUSE	08bbx86_mus_musculu
33	321	4.3	551	2	Q6nvf9_MOUSE	06nvf9_mus_musculu
34	319	4.2	825	2	Q759h3_NEUCR	0759h3_neurospora
35	317.5	4.2	552	2	Q8W8H_PONPY	05vh8_pongo_pygma
36	316	4.2	551	2	Q5ES1_HUMAN	05381_homo_sapien
37	316	4.2	551	2	Q16630_HUMAN	016630_homo_sapien
38	315	4.2	249	1	RNC_BACSU	P51833_bacillus_su
39	311.5	4.2	528	2	Q45065_TEETNG	045q65_tetradon_n
40	310	4.1	548	2	Q6Dw4_XENLA	06ddw4_xenopus_lae
41	310	4.1	551	2	Q52134_CHICK	052134_gallus_gall
42	309.5	4.1	1604	2	Q7KQ14_ORYSA	Q7xq14_oryza_sativ
43	308.5	4.1	245	1	RNC_BACCR	Q819v8_bacillus_ce
44	307.5	4.1	229	1	RNC_LISM0	QBY691_listeria_mo
45	307.5	4.1	245	1	RNC_BACAN	Q8iw18_bacillus_an



Qy	241 GRRHRSLRREGRSPDRRQDSRVSRYSDYDRGTPSRHSYVERSREVERRRHRDRRS	300	Oy	1321 ENGAAMOLEKNPONAHQRFIGCRXQELKEMWEREHOEREPDTEIKK 1374
Db	241 GRRHRSLRREGRSPDRRQDSRVSRYSDYDRGTPSRHSYVERSREVERRRHRDRRS	300	Db	1321 ENGAAMOLEKNPONAHQRFIGCRXQELKEMWEREHOEREPDTEIKK 1374
Qy	301 PSLERSYKEYRSGRSGSYLSVPEPAGCTPPLGETIKNTDSWAPPLEIVNHRSTSREK 360		RESULT 2	
Db	301 PSLERSYKEYRSGRSGSYLSVPEPAGCTPPLGETIKNTDSWAPPLEIVNHRSTSREK 360		ID	O5HZJ0_MOUSE PRELIMINARY;
Qy	361 KARWESEKDRSDNSGSKDKNYTSKEKEETMDKNEEEELKPKWIRCHSEN 420		ID	O5HZJ0_MOUSE PRELIMINARY; PRT; 1373 AA.
Db	361 KARWESEKDRSDNSGSKDKNYTSKEKEETMDKNEEEELKPKWIRCHSEN 420		AC	O5HZJ0_
Qy	421 YSSSDPKDQVGISTVWGTSLRDLYKPEEEGSRQEAKAARPPWPKTKLDELESS 480		DT	O5HZJ0_ (TREMBLrel. 30; Last sequence update)
Db	421 YSSSDPKDQVGISTVWGTSLRDLYKPEEEGSRQEAKAARPPWPKTKLDELESS 480		DT	10-MAY-2005 (TREMBLrel. 30; Last annotation update)
Qy	481 SSECESDEDSTCSSSDSEVDTIASTIKRKAHPDRDLHDELYWNDGQMDGPKCSA 540		DT	10-MAY-2005 (TREMBLrel. 30; Last annotation update)
Db	481 SSECESDEDSTCSSSDSEVDTIASTIKRKAHPDRDLHDELYWNDGQMDGPKCSA 540		DE	Rnasen protein.
Qy	541 KURRGTRGHRSTPGEAIAKPCPMTNAGRLHYRITSPNPLDTRPTVEYDHEYI 600		GN	Name=Etch12; Synonym=Rnasen;
Db	541 KURRGTRGHRSTPGEAIAKPCPMTNAGRLHYRITSPNPLDTRPTVEYDHEYI 600		OS	Mus musculus (Mouse).
Qy	601 FEGFSMWAHAPITNIPACKVIRPNIDYTHFBBMMPENPCUGKLEPLSLIPDIBLY 660		OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Db	601 FEGFSMWAHAPITNIPACKVIRPNIDYTHFBBMMPENPCUGKLEPLSLIPDIBLY 660		OC	Mammalia; Eutheria; Buarchoptoglires; Gires; Rodentia; Sciurognathi;
Qy	661 DNWKGLPLFEDSPPPCCPFHEMPPFRFLPDPGCKEVISMHQLLYLILRCSKALVPERETIA 720		OC	Muroidea; Muridae; Murinae; Mus.
Db	661 DNWKGLPLFEDSPPPCCPFHEMPPFRFLPDPGCKEVISMHQLLYLILRCSKALVPERETIA 720		OX	NCBI_TAXID=10050;
Qy	721 NNLQWBLEWQYAECKGMITNTPGCKPSSRIDOLDRPDPNPDVTEPIVHFGIRPA 780		RN	[1]
Db	721 NNLQWBLEWQYAECKGMITNTPGCKPSSRIDOLDRPDPNPDVTEPIVHFGIRPA 780		RN	NUCLEOTIDE SEQUENCE.
Qy	781 QLSYAGDPOYQKLWKSYKLRHLLANSPKVOKTDQKLAQREBALQIKRQTMREVTY 840		RC	STRAT=C57BL/6; TISSUE=Brain;
Db	781 QLSYAGDPOYQKLWKSYKLRHLLANSPKVOKTDQKLAQREBALQIKRQTMREVTY 840		RC	MEMLINE=22388257; PubMed=1247932; DOI=10.1073/pnas.242603899;
Qy	841 ELSQGFWKGTGTRSDVQHAMMLALPVLTHTHRYQCLMHDKLIGYTFDRCILQAMTHP 900		RA	Straubhaar R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Db	841 ELSQGFWKGTGTRSDVQHAMMLALPVLTHTHRYQCLMHDKLIGYTFDRCILQAMTHP 900		RA	Klauser R.D., Collins F.S., Wagner L., Shemmer C.M., Schuler G.D.,
Qy	901 SHHLNFGMNPDIARNSLNCGRQPKYGRDKRHMNRKGKGNLNTLNMSLQGDPTPS 960		RA	Altshull S.F., Zebeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Db	901 SHHLNFGMNPDIARNSLNCGRQPKYGRDKRHMNRKGKGNLNTLNMSLQGDPTPS 960		RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Qy	961 RINHNERLEFLGDAVVEPLTSYLYLPPSLLEGGLATYRITAVONQHLMALKELDP 1020		RA	Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
Db	961 RINHNERLEFLGDAVVEPLTSYLYLPPSLLEGGLATYRITAVONQHLMALKELDP 1020		RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schatz T.B.,
Qy	1021 FMLYAHGPDLCRESDLRHAMANCFEAIGAVYLEGSLSLEAKOKLGRFLNDPDLREWLN 1080		RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Db	1021 FMLYAHGPDLCRESDLRHAMANCFEAIGAVYLEGSLSLEAKOKLGRFLNDPDLREWLN 1080		RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Qy	1081 YPLHPIQLOQEPDQIETSPVQLQTEFEAIGAVYLEGSLSLEAKOKLGRFLNDPDLREWLN 1140		RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Db	1081 YPLHPIQLOQEPDQIETSPVQLQTEFEAIGAVYLEGSLSLEAKOKLGRFLNDPDLREWLN 1140		RA	Villacon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Qy	1141 GHNORMEFLGDSIMQVATEVPIHFDHHEGHLTURSLVANRTOAKVAEELGNOBEA 1200		RA	Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Db	1141 GHNORMEFLGDSIMQVATEVPIHFDHHEGHLTURSLVANRTOAKVAEELGNOBEA 1200		RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Qy	1201 ITNDKTKRPGVGRKTTLADLIESFTALYDQLEVYHTFMNCFFPRLKEFFILNDWND 1260		RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Db	1201 ITNDKTKRPGVGRKTTLADLIESFTALYDQLEVYHTFMNCFFPRLKEFFILNDWND 1260		RA	Rodriguez A.C., Grimwood J.J., Schmutz J., Myers R.M.,
Qy	1261 PKSQLOQCLTRTTEGKEPDLYKLTQTVPSHARTYTVAMYKGRIGGGKSIQOA 1320		RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smialius D.E.,
Db	1261 PKSQLOQCLTRTTEGKEPDLYKLTQTVPSHARTYTVAMYKGRIGGGKSIQOA 1320		RA	Schnesch A., Scheine J.E., Jones S.J.M., Marra M.A.,
Qy	1261 PKSQLOQCLTRTTEGKEPDLYKLTQTVPSHARTYTVAMYKGRIGGGKSIQOA 1320		RT	'Generation and initial analysis of more than 15,000 full-length human
Db	1261 PKSQLOQCLTRTTEGKEPDLYKLTQTVPSHARTYTVAMYKGRIGGGKSIQOA 1320		RT	and mouse cDNA sequences", Proc. Natl. Acad. Sci. U.S.A. 99:1689-16903 (2002).
Qy	961 RINHNERLEFLGDAVVEPLTSYLYLPPSLLEGGLATYRITAVONQHLMALKELDP 1020		RL	[2]
Db	961 RINHNERLEFLGDAVVEPLTSYLYLPPSLLEGGLATYRITAVONQHLMALKELDP 1020		RL	NUCLEOTIDE SEQUENCE.
Qy	961 RINHNERLEFLGDAVVEPLTSYLYLPPSLLEGGLATYRITAVONQHLMALKELDP 1020		RG	NIH MCC Project; Submitted (JAN 2005) to the EMBL/GenBank/DDBJ databases.
Db	961 RINHNERLEFLGDAVVEPLTSYLYLPPSLLEGGLATYRITAVONQHLMALKELDP 1020		RG	EMBL: BC088999; AAH08999_1; "-; mRNA.
Qy	961 RINHNERLEFLGDAVVEPLTSYLYLPPSLLEGGLATYRITAVONQHLMALKELDP 1020		DR	Ensembl: ENSMUSG00000022191; Mus musculus.
Db	961 RINHNERLEFLGDAVVEPLTSYLYLPPSLLEGGLATYRITAVONQHLMALKELDP 1020		DR	MGI: MGI:1261425; Rnasen.
Qy	1021 FMLYAHGPDLCRESDLRHAMANCFEAIGAVYLEGSLSLEAKOKLGRFLNDPDLREWLN 1080		DR	C: intracellular; IEA.
Db	1021 FMLYAHGPDLCRESDLRHAMANCFEAIGAVYLEGSLSLEAKOKLGRFLNDPDLREWLN 1080		DR	GO; GO:0005622; C: double-stranded RNA binding; IEA.
Qy	1081 YPLHPIQLOQEPDQIETSPVQLQTEFEAIGAVYLEGSLSLEAKOKLGRFLNDPDLREWLN 1140		DR	GO; GO:0003725; F: double-stranded RNA binding; IEA.
Db	1081 YPLHPIQLOQEPDQIETSPVQLQTEFEAIGAVYLEGSLSLEAKOKLGRFLNDPDLREWLN 1140		DR	GO; GO:0004525; F: ribonuclease III activity; IEA.
Qy	1140 YPLHPIQLOQEPDQIETSPVQLQTEFEAIGAVYLEGSLSLEAKOKLGRFLNDPDLREWLN 1140		DR	P: RNA processing; IEA.
Db	1140 YPLHPIQLOQEPDQIETSPVQLQTEFEAIGAVYLEGSLSLEAKOKLGRFLNDPDLREWLN 1140		DR	Inter-Pro; IPR00099; RNase_III.
Qy	1140 YPLHPIQLOQEPDQIETSPVQLQTEFEAIGAVYLEGSLSLEAKOKLGRFLNDPDLREWLN 1140		DR	Pfam; PF00035; dRm; I.
Db	1140 YPLHPIQLOQEPDQIETSPVQLQTEFEAIGAVYLEGSLSLEAKOKLGRFLNDPDLREWLN 1140		DR	Pfam; PF00636; Ribonuclease_3_2.
Qy	1140 YPLHPIQLOQEPDQIETSPVQLQTEFEAIGAVYLEGSLSLEAKOKLGRFLNDPDLREWLN 1140		DR	SMART; SM00358; dRm; I.
Db	1140 YPLHPIQLOQEPDQIETSPVQLQTEFEAIGAVYLEGSLSLEAKOKLGRFLNDPDLREWLN 1140		DR	SMART; SM0035; Riboc; 2.
Qy	1140 YPLHPIQLOQEPDQIETSPVQLQTEFEAIGAVYLEGSLSLEAKOKLGRFLNDPDLREWLN 1140		DR	PROSITE; PS00517; RmSE_3_1; 2.
Db	1140 YPLHPIQLOQEPDQIETSPVQLQTEFEAIGAVYLEGSLSLEAKOKLGRFLNDPDLREWLN 1140		DR	PROSITE; PS50142; RmSE_3_2; 2.
Qy	1201 ITNDKTKRPGVGRKTTLADLIESFTALYDQLEVYHTFMNCFFPRLKEFFILNDWND 1260		DR	PROSITE; PS50143; RmSE_3_2; 2.
Db	1201 ITNDKTKRPGVGRKTTLADLIESFTALYDQLEVYHTFMNCFFPRLKEFFILNDWND 1260		DR	Query Match 95.5%; Score 7160; DB 2; Length 1373;
Qy	1201 ITNDKTKRPGVGRKTTLADLIESFTALYDQLEVYHTFMNCFFPRLKEFFILNDWND 1260		DR	Best Local Similarity 95.3%; Pred. No. 0;
Qy	1261 PKSQLOQCLTRTTEGKEPDLYKLTQTVPSHARTYTVAMYKGRIGGGKSIQOA 1320		DR	Matches 1310; Conservative 32; Mismatches 30; Indels 2; Gaps 2;
Db	1261 PKSQLOQCLTRTTEGKEPDLYKLTQTVPSHARTYTVAMYKGRIGGGKSIQOA 1320		DR	2 MCQNTCHRMSFRGRGCPGRGRRGKGRAPSFRPONLRLHQQPPVQYEPSSAPST 61

Db	1	MGCGNTCHRMSTIPGRGCPRGGGGHARPSAFAFRPQNRLIHPQOQPAQTYEPPSAPSS	60	Qy	1141	GNHORMEFLGDSIMOLVATELETHPDRHGHGLTLRSLSVNRTOAQYAEELMQEYA	1200
Qy	62	TFNSNSPAPNPLFPLPRPDTPVPPFPMPMPSAQGPILPPCPTRPPEPNHOMRHPFPFPMP	121	Db	1140	GNHORMEFLGDSIMOLVATELETHPDRHGHGLTLRSLSVNRTOAQYAEELMQEYA	1199
Db	61	SYNSNSOAPSFWEPRPDPFVYPPPAFAAFAAQSQGLFPPCFVRPPYFNHOMRHPFPFPMP	120	Qy	1201	ITNDKTKRPGVLRKTILADLESFALYKDKOLEYHHTMNCVCPRLKEFILQDWDN	1260
Qy	122	PPMPMCNNPPVPGAPGQGTPFMMPPSMPMPPRPPRPPVMPQOQNTQYPPGSHINHPPPS	181	Db	1200	ITNDKTKRPGVLRKTILADLESFALYKDKOLEYHHTMNCVCPRLKEFILQDWDN	1259
Db	121	PPMPCPNPPAGSAPPQGTPFMPVPPSMPPVPPVMPVMPQOQNTQYPPGSHINHPPPS	179	Qy	1261	PKS0QOCCTLRTECKEPPDILYKTLQTVGSHARTTYTAWYFGCBIGGKGS1Q0	1320
Qy	182	FNSFQNNPSSFLPSANSSSPHFRHPPYPLKAPSERRSERLKYDHRHRSRHSRG	241	Db	1260	PKS0QOCCTLRTECKEPPDILYKTLQTVGSHARTTYTAWYFGCBIGGKGS1Q0	1319
Db	180	FNSYQNNSSSFPSANSSTSPPFRHPPYPLKAPSERRSERLKYDHRHRSRHSRG	239	Qy	1321	EMGAANDALEKNPOMAHOKEFGRKRYOELKMRWEREHOEREPDETDIKK	1374
Qy	242	ERHRSIDRERRGRSPDRRQDOSRSYSDYDGET-PSRHSVERSRRERERERHRHRSRHSRG	300	Db	1320	EMGAANDALEKNPOMAHOKEFGRKRYOELKMRWEREHOEREPDETDIKK	1373
Db	240	ERHRSIDRERRGRSPERRPSPRSYRSYDGETTPPRHRSRHSRDRERHRHRSRHSRG	299				
Qy	301	PSLERSYKKEYRSRGSYGSYLSVPEPGCTBLPGELIKNTDSWAPPLETINHRSRHSRG	360				
Db	300	PSLERSYKKEYRSRGSYGSYLSVPEPGCTBLPGELIKNTDSWAPPLETINHRSRHSRG	359				
Qy	361	KEARWEEKEDRWSDSQSGSKERNTSKEKEPTEWDKNEEEBELLKPYWIRCHSEN	420				
Db	360	KEARWEEKEDRWSDSQSGSKERNTSKEKEPTEWDKNEEEBELLKPYWIRCHSEN	419	DT	05-JUL-2004 (Tremblrel. 27, Last sequence update)		
Qy	421	YSSSDPMQVGSDSTVGTSLRRLDLYKFEELIGSRSOKAKARPPWEPPTKILKDELESS	480	DE	Rnase protein (Fragment)		
Db	420	YSSSDPMQVGSDSTVGTSLRRLDLYKFEELIGSRSOKAKARPPWEPPTKILKDELESS	479	GN	Name-Etch2; Synonyms=Rnase;		
Qy	481	SESECSDSDECCSSESSEVDPVIAKCPRTMINNAGRFLHYRTVSPPNFLDRPTWIEYDHEYI	600	OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Db	480	SESECSDSDECCSSESSEVDPVIAKCPRTMINNAGRFLHYRTVSPPNFLDRPTWIEYDHEYI	599	OC	Mammalia; Buteraria; Burchontoglies; Gires; Rodentia; Sciurognathi;		
Qy	541	KARTGIRHSYRGEAIAKCPRTMINNAGRFLHYRTVSPPNFLDRPTWIEYDHEYI	600	OC	Muroidea; Muridae; Murinae; Mus.		
Db	540	KARTGIRHSYRGEAIAKCPRTMINNAGRFLHYRTVSPPNFLDRPTWIEYDHEYI	599	OX	NCBI_TaxID=10090;		
Qy	550	DWNLKGPLFESSPPCCPFRFHFPRFPLGKEVLSMHOILLYLURCSKALVBEIA	720	RN	[1]		
Db	550	DWNLKGPLFESSPPCCPFRFHFPRFPLGKEVLSMHOILLYLURCSKALVBEIA	719	RP	RESULT 3		
Qy	601	FBGFSMFAHAPITNIPICKVIRFNIDTIEFTEBMMENFCUGKGLFSLFELFRDILEY	660	RC	Q6PA16_MOUSE PRELIMINARY; PRT: 1231 AA.		
Db	600	FBGFSMFAHAPITNIPICKVIRFNIDTIEFTEBMMENFCUGKGLFSLFELFRDILEY	659	RC	Q6PA16_MOUSE PRELIMINARY; PRT: 1231 AA.		
Qy	721	NMLOQWELEWQCYAECKGMIYTNPCTKPSSTIDOLDRDREPPNPDVITPITVHGRPA	780	RC	NUCLEOTIDE SEQUENCE.		
Db	720	NMLOQWELEWQCYAECKGMIYTNPCTKPSSTIDOLDRDREPPNPDVITPITVHGRPA	779	RC	NUCLEOTIDE SEQUENCE.		
Qy	781	QISYAGDPOQYQCLWKSVKLRLANSPVKVTKSVKLRLANSPVKVTKDOKLAQREBLQKIROQNTMRETV	840	RC	NUCLEOTIDE SEQUENCE.		
Db	780	QISYAGDPOQYQCLWKSVKLRLANSPVKVTKDOKLAQREBLQKIROQNTMRETV	839	RC	NUCLEOTIDE SEQUENCE.		
Qy	841	ELSSQGKWTGGRSDVQHAMMLPVLTTHIRHOCMLDKLIGYTFDRCQLQAMTHP	900	RC	NUCLEOTIDE SEQUENCE.		
Db	840	ELSSQGKWTGGRSDVQHAMMLPVLTTHIRHOCMLDKLIGYTFDRCQLQAMTHP	899	RC	NUCLEOTIDE SEQUENCE.		
Qy	901	SHHLNFGNNPDRARNLSNCGTROPKYGRKRVHMMRKGINTLNIMSGLQDPTPS	960	RC	NUCLEOTIDE SEQUENCE.		
Db	900	SHHLNFGNNPDRARNLSNCGTROPKYGRKRVHMMRKGINTLNIMSGLQDPTPS	959	RC	NUCLEOTIDE SEQUENCE.		
Qy	961	RINHNERLEPLGDAVVELTSHLYKIPSLLEGGLATYRIMVQHMLAKKELDP	1020	RC	NUCLEOTIDE SEQUENCE.		
Db	960	RINHNERLEPLGDAVVELTSHLYKIPSLLEGGLATYRIMVQHMLAKKELDP	1019	RC	NUCLEOTIDE SEQUENCE.		
Qy	1021	FMLYAHGPDLCKESDLRHAMACPFEAHLIGAVLIEGSLEAKOLFGRLLFNDDEBMLN	1080	RC	NUCLEOTIDE SEQUENCE.		
Db	1020	FMLYAHGPDLCKESDLRHAMACPFEAHLIGAVLIEGSLEAKOLFGRLLFNDDEBMLN	1079	RC	NUCLEOTIDE SEQUENCE.		
Qy	1081	YPLHPLQLOQPTDQRIETSPVLUQKLTTEFEEAIGVFTHRLAFTARTGENHML	1140	RC	NUCLEOTIDE SEQUENCE.		
Db	1080	YPLHPLQLOQPTDQRIETSPVLUQKLTTEFEEAIGVFTHRLAFTARTGENHML	1139	RC	NUCLEOTIDE SEQUENCE.		

DR	SMART: SM00358; DSRM: 1.	Db	900 CPEALIGAVILEGSLERKQFLGRLLFENDPDRREVNLYPLHQLQBPNTDROLIESP 959
DR	PROSITE; PS50137; DS RBD: 1.	Db	1103 VIQKLTTEREAGVIFHVRILARAFTRITQFGNHITLGHNORMEFLGDSMOLVATEYL 1162
DR	PROSITE; PS50517; RNASE_3_1; 2.	Db	960 VIQKLTTEREAGVIFHVRILARAFTRITQFGNHITLGHNORMEFLGDSMOLVATEYL 1019
FT	FTN TRR 1	SQ	SEQUENCE 1231 AA; 143573 MW; 3679FA987800151 CRC64;
Query	Match 85.1%; Score 6380; DB 2; Length 1231;	Query	Match 84.6%; Score 6344.5; DB 2; Length 1336;
Best Local Similarity 96.1%; Pred. No. 2 9e-303; Matches 1184; Conservative 22; Mismatches 24; Indels 2; Gaps 2;	Best Local Similarity 85.3%; Pred. No. 1 7e-301; Matches 1171; Conservative 76; Mismatches 81; Indels 45; Gaps 5;		
Db	1 FNVPPPSMPPRPPPPVQVNVQPGCYSHNFPQPSFNQNNSPSFLSGANNSSPH 203	Db	1043 CPEALIGAVILEGSLERKQFLGRLLFENDPDRREVNLYPLHQLQBPNTDROLIESP 959
Qy	144 FMPPPPSMPPRPPPPVQVNVQPGCYSHNFPQPSFNQNNSPSFLSGANNSSPH 203	Qy	1163 FHPDPDHEGHITLRLSSLVNRTQAKVAEIGMQEYAITNDKTPVGLRTKLADLE 1222
Db	1 FNVPPPSMPPRPPPPVQVNVQPGCYS-HSPPPGPNSTQNNSSPPRANSSTPH 59	Db	1020 FHPDPDHEGHITLRLSSLVNRTQAKVAEIGMQEYAITNDKTPVGLRTKLADLE 1079
Qy	204 FHLHPPVPLPKPSRASPERLKYDDEHRHRSRHSRGRHRSRSLDRBERGRPDRRQDS 263	Qy	1223 SFIAALYTDKOLIYVHFMNVCFFPRLKEFTILQDNDPKSQLQQCCITLRTGKEDIP 1282
Db	60 FHLHPPVPLPKPSRASPERLKYDDEHRHRSRGRHRSRSLDRBERGRPDRRQDS 263	Db	1080 SFIAALYTDKOLIYVHFMNVCFFPRLKEFTILQDNDPKSQLQQCCITLRTGKEDIP 1139
Qy	264 RYSDYDRGRT-PSRHSYERSRERERBRHRDRNRNRSPLSLRSYKEYKRGGRSGSYLSV 322	Qy	1283 LYKLTQWGSARTHTWAVFGERIGGGKPSIQAEMGRDAMALEKYNPQMAHQR 1342
Db	120 RYSDYDRGRT-PSRHSYERSRERERBRHRDRNRNRSPLSLRSYKEYKRGGRSGSYLSV 179	Db	1140 LYKLTQWGSARTHTWAVFGERIGGGKPSIQAEMGRDAMALEKYNPQMAHQR 1199
Qy	323 VEPAGCTPELGEIINTDSWAPPLEVNRHSPRSERKARWEEKDWSNQSSDK 382	Qy	1343 FIGRKTRQBLKMRWERHQEREPDEDIKK 1374
Db	180 AEPAGCTPELGEIINTDSWAPPLEVNRHSPRSERKARWEEKDWSNQSSDK 239	Db	1200 FICKYKQELKMRWERHQEREPDEDIKK 1231
Qy	383 NTTSIKEKEPESTMPDKNQEEBEBBLKPWVWICTHSENYYSSDPMDOVGSTDWGSRLR 442	RESULT 4	
Db	240 NTTSIKEKEAEVPPKTEERERBRERBLKPWVWICTHSENYYSSDPMDOVGSTDWGSRLR 299	Q5ZIR3 CHICK	
Qy	443 DYYDKFREBELGSRSOEKAKAARPPWERPKTKLUDBLESSESSESSTCESDSDSTESSSSSEVF 502	ID	Q5ZIR3-CHICK PRELIMINARY; PRT; 1336 AA.
Db	300 DJYDKFREBELGSRSOEKAKAARPPWERPKTKLUDBLESSESSESSTCESDSDSTESSSSSEVF 359	DT	05ZIR3 (TREMBrel. 28, Last sequence update)
Qy	503 DVIATEIKRKKAAPDRLDELWNPQGMDNGLCKSOSAKARTGIRHSYPEEAKPCR 562	DT	25-OCT-2004 (TREMBrel. 28, Last sequence update)
Db	360 DVIATEIKRKKAAPDRLDELWNPQGMDNGLCKSOSAKARTGIRHSYPEEAKPCR 419	DE	Hypothetical protein.
Qy	563 PTMNNAGRLFHYITISPPNTNLTDRTVIEDDHEITPEGESMAHAPLTIPLCKV 622	GN	RENames=RCUMB04_24aa1;
Db	420 PTMNNAGRLFHYITISPPNTNLTDRTVIEDDHEITPEGESMAHAPLTIPLCKV 479	OS	Gallus gallus (Chicken).
Qy	623 FMDYTHFIERKMPENPCVKGKELFSLFSLPFRDILEYDWNNGKGPLFEDSPCCPRPHM 682	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; OC
Db	480 FMDYTHFIERKMPENPCVKGKELFSLFSLPFRDILEYDWNNGKGPLFEDSPCCPRPHM 539	OC	Gallus; Gallus; Galliformes; Phasianidae; Phasianinae; OC
Qy	683 PRFVRFLPDDGGEVLSHQIYLRLRSKALPEEFTANMOWEELEWQKAYECKGMIV 742	RN	NCBI_TAXID=9031; [1]
Db	540 PRFVRFLPDDGGEVLSHQIYLRLRSKALPEEFTANMOWEELEWQKAYECKGMIV 599	RP	NUCLEOTIDE SEQUENCE.
Qy	743 TPGTKESSVRDQDQRFQNFQDIDVITPIVFGIRPAQLSAGDPOYOKWVSKYKLRH 802	RC	STRAIN=CB; TISSUE=Bursa; Caldwell R. B., Kierke A. M., Arakawa H., Bezzubov Y., Zaim J., RA
Db	600 TPGTKESSVRDQDQRFQNFQDIDVITPIVFGIRPAQLSAGDPOYOKWVSKYKLRH 659	RA	Fiedler P., Kutter S., Blagodatski A., Kostovska D., Kotter M., RA
Qy	803 LIANSPKVKQTKQKQKLAQREELQKIRQNTTREVTVELSSQGFWTGTGIRSDVCOHAMM 862	RT	Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.; RT
Db	660 LIANSPKVKQTKQKQKLAQREELQKIRQNTTREVTVELSSQGFWTGTGIRSDVCOHAMM 719	RL	genefunction analysis"; Genome Biol. 6:R6-R6(2005).
Qy	863 LPVLTTHIRYHSCMLMHDKLKGTYFQDCLQOLAMTHPSHUNFGMNPDHARNSLNGI 922	DR	EMLB; AW720721; CAG2380.1; -; mRNA.
Db	720 LPVLTTHIRYHSCMLMHDKLKGTYFQDCLQOLAMTHPSHUNFGMNPDHARNSLNGI 779	DR	DR; GO; 0005634; C:nucleus; IEA.
Qy	923 RQPKYGRKVKVHMHRKGKINTLNLINMSRLGDPPTSRINNBRLEPLGDAWELTSV 982	DR	DR; GO; 0003725; F:double-stranded RNA binding; IEA.
Db	780 RQPKYGRKVKVHMHRKGKINTLNLINMSRLGDPPTSRINNBRLEPLGDAWELTSV 839	DR	DR; GO; 0004519; F:endonuclease activity; IEA.
Qy	983 HYYLFLPSLEEGLGLATRTATVONOHIALMACKLEDPFMLVLAHGPDLCLRSRDLRHAMM 1042	DR	DR; GO; 0016787; F:hydrolase activity; IEA.
Db	840 HYYLFLPSLEEGLGLATRTATVONOHIALMACKLEDPFMLVLAHGPDLCLRSRDLRHAMM 899	DR	DR; GO; 0004525; F:ribonuclease III activity; IEA.
Qy	1043 CPEALIGAVILEGSLERKQFLGRLLFENDPDRREVNLYPLHQLQBPNTDROLIESP 1102	DR	DR; GO; 000396; F:RNA processing; IEA.
Db	1 MSFHPRGRCGPGRGGHGRPSAPSFRPQNLHPOQPVQYQEPSPASTPSNSPAP 69	DR	DR; InterPro; IPR001159; DS RBD; 1.
Qy	10 MSFHPRGRCGPGRGGHGRPSAPSFRPQNLHPOQPVQYQEPSPASTPSNSPAP 69	DR	DR; InterPro; IPR000999; RNase_III.
Db	1 MSFHPRGRCGPGRGGHGRPSAPSFRPQNLHPOQPVQYQEPSPASTPSNSPAP 69	DR	DR; Pfam; PF00636; darm; 1.
Qy	10 MSFHPRGRCGPGRGGHGRPSAPSFRPQNLHPOQPVQYQEPSPASTPSNSPAP 69	DR	DR; Pfam; PF00358; DSRM; 1.
Db	1 MSFHPRGRCGPGRGGHGRPSAPSFRPQNLHPOQPVQYQEPSPASTPSNSPAP 69	DR	DR; SMART; SM00353; RIBOC; 2.
Qy	10 MSFHPRGRCGPGRGGHGRPSAPSFRPQNLHPOQPVQYQEPSPASTPSNSPAP 69	DR	DR; PROSITE; PS50137; DS RBD; 1.
Db	1 MSFHPRGRCGPGRGGHGRPSAPSFRPQNLHPOQPVQYQEPSPASTPSNSPAP 69	DR	DR; PROSITE; PS50517; RNase_3_1; 2.
Qy	10 MSFHPRGRCGPGRGGHGRPSAPSFRPQNLHPOQPVQYQEPSPASTPSNSPAP 69	DR	DR; PROSITE; PS50142; RNase_3_2; 2.
Db	1 MSFHPRGRCGPGRGGHGRPSAPSFRPQNLHPOQPVQYQEPSPASTPSNSPAP 69	KW	Hypothetical protein.
Qy	10 MSFHPRGRCGPGRGGHGRPSAPSFRPQNLHPOQPVQYQEPSPASTPSNSPAP 69	SQ	SEQUENCE 1336 AA; 154836 MW; 5D9A9A9C53DE0CF CRC64;
Query	Match 84.6%; Score 6344.5; DB 2; Length 1336;	Query	Match 85.1%; Score 6380; DB 2; Length 1231;
Best Local Similarity 85.3%; Pred. No. 1 7e-301; Matches 1171; Conservative 76; Mismatches 81; Indels 45; Gaps 5;	Best Local Similarity 85.3%; Pred. No. 2 9e-303; Matches 1184; Conservative 22; Mismatches 24; Indels 2; Gaps 2;		

Db	1104	HNORMEFLGDSIMQVAVLBFISFHDFHGHUJLRSLSLNUKQAVABEILSMMWAI
QY	1202	NDTCKTPVGLRTKTLADLESFIAVLYTQDKEVHTFMVNCFPRLKEFITNDQMDP
Db	1164	TNDKTKRPVLAFTKTLADLESFIAVLYTQDKEVHTFMVNCFPRLKEFITNDQMDP
QY	1262	KSQIQCQCTILRTPEGKEPIPLYKLTQVTPSHARYTIVAVYFGGRIGGGPSIQAE
Db	1224	KSQIQCQCTILRTPEGKEPIPLYKLTQVTPSHARYTIVAVYFGGRIGGGPSIQAE
QY	1322	MGAANDALEKYNFPQMAHOKRFIGKYRQELKEMWREHOBEPDTEIDK
Db	1284	MGAANDALEKYNFPQMAHOKRFIGKYRQELKEMWREHOBEPDTEIDK
RESULT 5		
OBOZ69	MOUSE	PRT; 1021 AA.
ID	QBOZ69_MOUSE	PRELIMINARY;
AC	QBOZ69;	
DT	01-JUN-2003	(Tremblrel. 24, Last sequence update)
DT	01-MAR-2004	(Tremblrel. 26, Last annotation update)
DE		ribonuclease III.
GN		Name=Etchiz; Synonyms=Rnasen;
OS		Mus musculus (Mouse).
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Rodentia; Muridae; Murinae; Mus.
OX		NCBI_TaxID=1090;
RN		[1]
RC		NUCLEOTIDE SEQUENCE.
RK		STRAIN=BALB/C; TISSUE=kidney;
RA		MEDLINE=22730749; PubMed=12191433;
RT		Fortin K.R., Nicholson R.H., Nicholson A.W.;
RT		"Mouse ribonuclease III. cDNA structure, expression analysis, and chromosomal location." BMC Genomics 3:26-26 (2002).
RL		EMBL: AP533013; AA065849.1; -; mRNA.
DR		HSRP; 067082; 1JFZ.
DR		Ensembl; ENSEMBL000022191; Mus musculus.
DR		MGI; MGI:1261425; Etchiz.
DR		MGI; MGI:1261425; Rnasen.
DR		GO; GO:0006522; Cytosolic; IEA.
DR		GO; GO:0003725; P_double-stranded_RNA_binding; IEA.
DR		GO; GO:0004525; Ribonuclease III activity; IEA.
DR		GO; GO:0006525; Ribonuclease III processing; IEA.
DR		InterPro; IPR01159; Ds_RNA_bd.
DR		InterPro; IPR000939; Rnasen_III.
DR		Pfam; PF00025; dsrm; 1.
DR		Pfam; PF00636; Ribonuclease_3; 2.
DR		SMART; SM00358; USRM; 1.
DR		SMART; SM00335; RIBOC; 2.
DR		PROSITE; PS50137; DS_RBD; 1.
DR		PROSITE; PS00517; RNASE_3_1; 2.
DR		PROSITE; PS50142; RNASE_3_2; 2.
SEQENCE		SEQUENCE 1021 AA: 116200 MW; 15E4899270A86F29 CRC64;



SEQUENCE	942 AA;	109445 MW;	C362946786C8CB CRC64;
Qy	STVGTGTSRUDLYKDFEEBLGSROEKAKARPPWEPKTLKDDLEESSESECESEDEBT	66.4%; Score 4982; DB 2; Length 942;	DT 01-OCT-2003 (TREMBL, 25, Created)
Best Local Similarity	98.9%; Pred. No. 4.1e-235;		DT 01-OCT-2003 (TREMBL, 25, Last sequence update)
Matches	932; Conservative 5; Mismatches 5; Indels 0; Gaps 0;		DT 01-MAR-2004 (TREMBL, 26, Last annotation update)
Qy	STVGTGTSRUDLYKDFEEBLGSROEKAKARPPWEPKTLKDDLEESSESECESEDEBT	60	DE Rnasen Protein (Fragment).
Qy	1 STVGTGTSRUDLYKDFEEBLGSROEKAKARPPWEPKTLKDDLEESSESECESEDEBT	60	GN Name=Etchii; Synonyms=Rnasen;
Qy	493 CSSSSSEVFVDAEIKRICKAHPDLHDLWYDNPQOMGPGICKSAKARRGCRHSTY	552	OS Mus musculus (Mouse);
Qy	61 CSSSSSEVFVDAEIKRICKAHPDLHDLWYDNPQOMGPGICKSAKARRGCRHSTY	552	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Qy	1 STVGTGTSRUDLYKDFEEBLGSROEKAKARPPWEPKTLKDDLEESSESECESEDEBT	552	OC Mammalia; Eutheria; Earchontoglires; Glires; Rodentia; Sciurognath;
Qy	553 PGEBAIKPCPMTNNAGRLPHYRITVSPPTNFLDRTPTVIEYDDHEYPEGFSMFAHPL	612	OC Muroidea; Muridae; Murinae; Mus.
Qy	121 PGEBAIKPCPMTNNAGRLPHYRITVSPPTNFLDRTPTVIEYDDHEYPEGFSMFAHPL	612	OC NCBI_TaxID=1090;
Db	613 TNPLICKVRFNIDTYTHFTEEMMPBNPCVKGLFSLFLFRLTLEDTWNLKGPFEDS	672	RN [1]
Db	181 TNPLICKVRFNIDTYTHFTEEMMPBNPCVKGLFSLFLFRLTLEDTWNLKGPFEDS	672	RP NUCLEOTIDE SEQUENCE.
Db	673 PPGCFPRFHMPRFVFLPGGKEVLSMHQILLYLURCSKALVBEIANLQBELENQ	732	RC STRAIN=57BL/6; TISSUE=Mouse;
Db	241 PPGCFPRFHMPRFVFLPGGKEVLSMHQILLYLURCSKALVBEIANLQBELENQ	732	RX MEDLINE=22338257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Db	733 YABECKGMIVTNPGKTPKSSVRIDDLRDEQFNPDTIPTPIVHGRIRPAOLSYAGDPQYQK	792	RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Db	301 YABECKGMIVTNPGKTPKSSVRIDDLRDEQFNPDTIPTPIVHGRIRPAOLSYAGDPQYQK	792	RA Klausner R.D., Collins F.S., Wagner L., Shremmen C.M., Schuler G.D.,
Qy	793 LWKSYVKLRLHLLANSPPKVKOTDKKLAQOEAROKTRONTMREYVTELSSGGFWKGIGI	852	RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Blatt N.K.,
Qy	361 LWKSYVKLRLHLLANSPPKVKOTDKKLAQOEAROKTRONTMREYVTELSSGGFWKGIGI	852	RA Hopkins R.P., Jordan H., Moore T., Max S.J., Wang J., Hsieh F.,
Qy	853 RSDVQOHAMMLPVLTHIRYHQCLMHDKIGYFQDCLQLAMTHSHLNFGMNIDH	912	RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.E.,
Qy	421 RSDVQOHAMMLPVLTHIRYHQCLMHDKIGYFQDCLQLAMTHSHLNFGMNIDH	912	RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C.,
Db	913 ARNSLSNCGTRQPKGDKRYHMMRKGGINTLNTMSRLGDDPTPSRINHNERLEFIG	972	RA Brownstein M.J., Usdin T.B., Yoshiuki S., Carninci P., Abramson R.D., Mullaney S.J.,
Db	481 ARNSLSNCGTRQPKGDKRYHMMRKGGINTLNTMSRLGDDPTPSRINHNERLEFIG	972	RA Rana S.S., Loquellano N.A., Petters G.J.J., Dickson M.C.,
Qy	973 DAVVPLTSVHLYLIPPSLEGGIATYRPIVQHQLAMLAKKLEDPMPYAHGPDICR	1032	RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Qy	541 DAVVPLTSVHLYLIPPSLEGGIATYRPIVQHQLAMLAKKLEDPMPYAHGPDICR	1032	RA Richards S., Worley K.C., Garcia A.M., Gay L.J., Hulyk S.W.,
Db	1033 ESDLRHMANCFAEALIGAVYLEGSLEAKQFLGRILFNDPDLREWMLNPLHQLQOPEN	1092	RA Villalon D.K., Mazny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Db	601 ESDLRHMANCFAEALIGAVYLEGSLEAKQFLGRILFNDPDLREWMLNPLHQLQOPEN	1092	RA Fahy J., Heaton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
Qy	1093 TDROLIETSPVQKQUTEFEEAIGVFTHMLTGHNORMEFLGDS	1152	RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Db	661 TDROLIETSPVQKQUTEFEEAIGVFTHMLTGHNORMEFLGDS	1152	RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Qy	1153 IMQVATEWIFHDPHECHLTURSLSSUNRQAKVABEILQGQYAITNDKTRKPGI	1212	RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Db	721 IMQVATEWIFHDPHECHLTURSLSSUNRQAKVABEILQGQYAITNDKTRKPGI	1212	RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smilus D.E.,
Db	1213 RTKTAIDLIESFIAALYDQKLEVYHPTMNCFFPLKFTILNDNDKPSLQOCCLTL	1272	RA Schmrich A., Schein J.E., Jones S.J.M., Marra M.A.,
Qy	781 RTKTAIDLIESFIAALYDQKLEVYHPTMNCFFPLKFTILNDNDKPSLQOCCLTL	1272	RT "Generation and initial analysis of more than 15,000 full-length human
Db	1273 RTEGKEPDPLYKTDQTVGSHARYTAVYKGERIGCGKGS1QQAEMGAADALEY	1332	RT and mouse cDNA sequences.",
Qy	841 RTEGKEPDPLYKTDQTVGSHARYTAVYKGERIGCGKGS1QQAEMGAADALEY	900	RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
Db	901 NFPQMAHQKFRIGRYXRQEIKEMRVREREREPDTEDEIKK	942	RL RN [2]
Qy	RESULT 7 QTMW8 MOUSE		RP
Qy	SEQUENCE		NUCLEOTIDE SEQUENCE.
Qy	STRAIN=57BL/6; TISSUE=Mouse;		RC STRAIN=C57BL/6; TISSUE=Mouse;
Qy	NIH MGC Project;		RG NIH MGC Project;
Qy	Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.		RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
Db	EMBL; BC055696; AAH55696.1; -; mRNA.		DR EMBL; BC055696; AAH55696.1; -; mRNA.
Qy	ENSEMBL; ENSGUS0000022191; Mus musculus.		DR ENSEMBL; ENSGUS0000022191; Mus musculus.
Db	MGI; MGI:1261425; Ettoh2.		DR MGI; MGI:1261425; Ettoh2.
Qy	1093 TDROLIETSPVQKQUTEFEEAIGVFTHMLTGHNORMEFLGDS	1152	DR GO; GO:0005622; C:intracellular; IEA.
Db	661 TDROLIETSPVQKQUTEFEEAIGVFTHMLTGHNORMEFLGDS	1152	DR GO; GO:0004525; F:ribonuclease-III activity; IEA.
Qy	1153 IMQVATEWIFHDPHECHLTURSLSSUNRQAKVABEILQGQYAITNDKTRKPGI	1212	DR GO; GO:0006396; P:RNA processing; IEA.
Db	721 IMQVATEWIFHDPHECHLTURSLSSUNRQAKVABEILQGQYAITNDKTRKPGI	1212	DR InterPro; IPR001159; Da RNA bd.
Db	1213 RTKTAIDLIESFIAALYDQKLEVYHPTMNCFFPLKFTILNDNDKPSLQOCCLTL	1272	DR InterPro; IPR000999; RNase_III.
Qy	781 RTKTAIDLIESFIAALYDQKLEVYHPTMNCFFPLKFTILNDNDKPSLQOCCLTL	1272	DR Pfam; PF00035; dsm;
Db	1273 RTEGKEPDPLYKTDQTVGSHARYTAVYKGERIGCGKGS1QQAEMGAADALEY	1332	DR Pfam; PF00636; Ribonuclease_3;
Qy	841 RTEGKEPDPLYKTDQTVGSHARYTAVYKGERIGCGKGS1QQAEMGAADALEY	900	DR SMART; SM00359; DSRM; 1.
Db	901 NFPQMAHQKFRIGRYXRQEIKEMRVREREREPDTEDEIKK	942	DR SMART; SM00355; RIBOC; 2.
Qy	RESULT 7 QTMW8 MOUSE		DR PROSITE; PS0137; DS RBD; 1.
Qy	SEQUENCE		DR PROSITE; PS00517; RNASE_3; 1; 2.
Db	901 NFPQMAHQKFRIGRYXRQEIKEMRVREREREPDTEDEIKK	942	DR PROSITE; PS50142; RNASE_3; 2; 2.
Qy	595 DDMHIFEGFSMFAHPLNTIPICKVRFNIDTYTHFTEEMMPBNPCVKGLFELFLR	654	FT NON_TER 1
Qy	1 DDMHIFEGFSMFAHPLNTIPICKVRFNIDTYTHFTEEMMPBNPCVKGLFELFLR	654	SQ SEQUENCE 780 AA; 91045 MW; 78D73433C75382B CRC64;
Qy	Query Match 54.9%; Score 4121; DB 2; Length 780;		Query Match 54.9%; Score 4121; DB 2; Length 780;
Best Local Similarity	99.1%; Pred. No. 3.8e-193;		Best Local Similarity 99.1%; Pred. No. 3.8e-193;
Matches	773; Conservative 2; Mismatches 5; Indels 0; Gaps 0;		Matches 773; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Qy	655 DILLYDNLKGPFLPESPPCCPFRHMPRFVPLPDGCKEVISWHQILLYLURCSKALV	714	Qy 655 DILLYDNLKGPFLPESPPCCPFRHMPRFVPLPDGCKEVISWHQILLYLURCSKALV
Qy	61 DILLYDNLKGPFLPESPPCCPFRHMPRFVPLPDGCKEVISWHQILLYLURCSKALV	714	Qy 61 DILLYDNLKGPFLPESPPCCPFRHMPRFVPLPDGCKEVISWHQILLYLURCSKALV

715 PEEETANLQEBELLENOYKABECKGMVITNGTKPSVRIDQDRQFNPDVITPFIHV 774  
 RA  
 181 FGIRPAQLSTAGDPQOKLWKSYVKLRLANSPKTYQTKDQKLAOREEALQKIRKNTM 834  
 RA  
 Db  
 121 PEEETANLQEBELLENOYKABECKGMVITNGTKPSVRIDQDRQFNPDVITPFIHV 180  
 RT  
 "Genome duplication in the teleost fish *Tetraodon nigroviridis* reveals  
 the early vertebrate proto-karyotype.";  
 Nature 431:946-957 (2004).  
 (2)  
 RN  
 NUCLEOTIDE SEQUENCE;  
 Genoscope; Whitehead Institute Centre for Genome Research;  
 Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.  
 -!- CAUTION: The sequence shown here is derived from an  
 EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is  
 preliminary data.  
 DR  
 EMBL; CAE0101565; CAE0101565; -; Genomic DNA,  
 SEQUENCE 1041 AA; 120534 MW; 2CA7A165A7BB3CDB CRC64;  
 SQ  
 RG  
 Query Match 50.2%; Score 3767; DB 2; Length 1041;  
 RL  
 Best Local Similarity 67.5%; Pred. No. 1.1e-175;  
 CC  
 Matches 738; Conservative 80; Mismatches 115; Indels 140; Gaps 18;  
 CC  
 Db  
 361 DDPTPSRINHNERLEFLGDAVTEFLTSVHLYTLPSPLEGGATYTAIVONOHJAMLK 360  
 QY  
 301 LAMTNPSPHHAFLGMDHARMSLSNGIROPKYQDKVHAMDMLKGINTLNLNRLQ 360  
 RT  
 835 RREVTTELSSOCFWKIGIRSPVQHAMMLPLTHRYHOCMHDMLKGINTLKGITFQDCLQ 894  
 QY  
 241 RREVTTELSSOCFWKIGIRSPVQHAMMLPLTHRYHOCMHDMLKGINTLKGITFQDCLQ 300  
 RN  
 775 FGIRPAQLSYGDPQOKLWKSYVKLRLANSPKTYQTKDQKLAOREEALQKIRKNTM 834  
 RA  
 895 LAMTNPSPHHAFLGMDHARMSLSNGIROPKYQDKVHAMDMLKGINTLNLNRLQ 954  
 RA  
 301 LAMTNPSPHHAFLGMDHARMSLSNGIROPKYQDKVHAMDMLKGINTLNLNRLQ 240  
 RT  
 955 DDPTPSRINHNERLEFLGDAVTEFLTSVHLYTLPSPLEGGATYTAIVONOHJAMLK 1014  
 QY  
 361 DDPTPSRINHNERLEFLGDAVTEFLTSVHLYTLPSPLEGGATYTAIVONOHJAMLK 420  
 QY  
 361 DDPTPSRINHNERLEFLGDAVTEFLTSVHLYTLPSPLEGGATYTAIVONOHJAMLK 420  
 QY  
 1015 KLELPPMFLYHGPOLCRESPLRHMANCEFALIGAVYLGSLKQLEKQFPLD 1074  
 QY  
 481 REWYNTPLPLQDQBPNTDQQLIGLSPVQKLEPTEAIGVITFVTRLLAFTURG 540  
 QY  
 421 KLELPPMFLYHGPOLCRESPLRHMANCEFALIGAVYLGSLKQLEKQFPLD 480  
 QY  
 1075 REWYNTPLPLQDQBPNTDQQLIGLSPVQKLEPTEAIGVITFVTRLLAFTURG 1134  
 QY  
 481 REWYNTPLPLQDQBPNTDQQLIGLSPVQKLEPTEAIGVITFVTRLLAFTURG 540  
 QY  
 1135 FNHLTIGHNRMEFGLDSIMOLVATEYLPFLHDPHNGHLLTURSLVNNRTOAKYAEEL 1194  
 QY  
 541 FNHLTIGHNRMEFGLDSIMOLVATEYLPFLHDPHNGHLLTURSLVNNRTOAKYAEEL 600  
 QY  
 1195 GMQEAIATNDKTKRPLVGLRTPLADLLESFALAYKDKDLYXVHNTMVEFPRKEFIL 1254  
 QY  
 601 GMQEAIATNDKTKRPLVGLRTPLADLLESFALAYKDKDLYXVHNTMVEFPRKEFIL 660  
 QY  
 1255 NQDWDPKS0QOCQCTLRLPCKEPPD1PLYKLTQVGPSHARTYVAVFKGERIGCGKG 1314  
 QY  
 661 NQDWDPKS0QOCQCTLRLPCKEPPD1PLYKLTQVGPSHARTYVAVFKGERIGCGKG 720  
 QY  
 1315 PSIOQAEEMGAAMDALKEYNPOMAOKRFFTERKYKROELKENVWERHOERBDETDIKK 1374  
 QY  
 721 PSIOQAEEMGAAMDALKEYNPOMAOKRFFTERKYKROELKENVWERHOERBDETDIKK 780  
 QY  
 RESULT 8  
 Q4KWL1 TETNG  
 ID Q4KWL1 TETNG PRELIMINARY; PRT; 1041 AA.  
 AC  
 Q5KWL1; 1, Created)  
 DT 13-SEP-2005 (TREMBREL. 31, Last sequence update)  
 DT 13-SEP-2005 (TREMBREL. 31, Last annotation update)  
 DE Chromosome undetermined SCAFF14565, whole genome shotgun sequence.  
 GN ORENAMES=GSTENG001653001; OS Tetraodon nigroviridis (Green puffer).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontidae; Tetraodon.  
 OC NCIN-TAXID=99883;  
 RN  
 RP NUCLEOTIDE SEQUENCE.  
 RA Jalil O., Aury J.M., Brunet F., Petit J.-L., Stange-Thomann N.,  
 RA Maucler E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
 RA Niclau S., Jaffe D., Fisher S., Lufalla G., Dosalat C., Segurens B.,  
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,  
 RA Bileont C., Shalli Z., Gattolico L., Poulain J., De Barardiniis V.,  
 RA Cruaud C., Durier S., Brottier P., Coustou J.-P., Gouzy J.,  
 RA Parra G., Lander G., Chapple C., McKernan K.J., McEwan P., Bosak S.,  
 RA Kelts M., Voigt J., Guigo R., Zody M.C., Mesirov J.,  
 RA Lindblad-Toh K., Birren B., Nusbaum D., Robinson-Rechavi M.,  
 RA  
 [1]  
 QY  
 439 SRLDPLDKEEELGSKQEKACARPWEPPTKLDL- ISSSESCESD-SCSS 496  
 QY  
 394 SKURDLQQRFEEBLGRQARACARPWEPPTKLDLSDPDESSESCEBESDAGSTCSS 453  
 QY  
 497 SDSEVEDVIAETKRGKAHPDIAHDELWINDQMDPLCKSOSAKARTGIRHSIMGEE 556  
 QY  
 454 SPSDSDVIAETKRGKAHPDIAHDELWINDQMDPLCKSOSAKARTGIRHSIYGE 513  
 QY  
 557 AJKPCRENTNAGLHYRTVSPPPTNLTQRTPTVYEDDHYIFEGFSMAMAPLTP 616  
 QY  
 514 SYKQCRAMANNAGLHYRTVSPPPTNLTQRTPTVYEDDHYIFEGFSMAMAPLTP 573  
 QY  
 617 ICKVIRENIDVTHFBEMMPLNFCVYGLELFSFLRDLIYDMLKGPFLFEDSPCC 676  
 QY  
 574 LCKVIRFNIDVTHFBEMTBNVYCVYGLELFSFLRDLIYDMLKGPFLFEDSPCC 633  
 QY  
 677 PREHMPMPFVFLPDKGKEVSMHQIYLJYURCSKALPVERBIANLQEWQYAE 736  
 QY  
 634 QPFHMPMPFVFLPDKGKEVSMHQIYLJYURCSKALPVERBIADLQWELEWQYAE 693  
 QY  
 737 CKGMIIVTNGPKPSSVRIDQDRQFNPDVITPPIVHFGIRPAOLSYAGDQYQKLUWS 796

RESULT 9

Db 694 CKGMIVTNPQGMKPPSRIDQDREQNPDVITFPIVHFGIRPAQLSYADPQIQKTLWS 753 DR GO; GO:004525; F:ribonuclease III activity; IEA. DR GO; GO:006396; P:RNA processing; IEA. DR InterPro; IPR011597; Ds RNA\_bd. DR InterPro; IPR00999; RNase\_III. DR Pfam; PF00035; drmi; 1. DR Pfam; PF00636; Ribonuclease\_3; 2. DR SMART; SM00358; DSRN; 1. DR SMART; SM00535; RBOC; 2. DR PROSITE; PS50137; DS\_RBD; 1. DR PROSITE; PS00517; RNASE\_3; 1; 2. DR PROSITE; PS50142; RNASE\_3\_2; 2. DR NON\_TER 1 1

SQ SEQUENCE 705 AA; 82084 MW; 3332C69A5F1977D6 CRC64;

Query Match Similarity 49.3%; Score 3666; DB 2; Length 705; Best Local Similarity 98.7%; Pred. No. 2e-172; 7; Mismatches 696; Conservative 2; Mismatches 7; Indels 0; Gaps 0; Matches 696; Conservative 2; Mismatches 7; Indels 0; Gaps 0; Matches 60

Db 874 LSNCGRQPKGDRKQHMHMKKGKQGINTLIMSLRGQDDPTPSRINHNERLEFGDAV 933 DR GO; GO:004525; F:ribonuclease III activity; IEA. DR GO; GO:006396; P:RNA processing; IEA. DR InterPro; IPR011597; Ds RNA\_bd. DR InterPro; IPR00999; RNase\_III. DR Pfam; PF00035; drmi; 1. DR Pfam; PF00636; Ribonuclease\_3; 2. DR SMART; SM00358; DSRN; 1. DR SMART; SM00535; RBOC; 2. DR PROSITE; PS50137; DS\_RBD; 1. DR PROSITE; PS00517; RNASE\_3; 1; 2. DR PROSITE; PS50142; RNASE\_3\_2; 2. DR NON\_TER 1 1

Db 814 CQHAMMLPVLTTHIRYHQCLMHDOLIGYVFTERCILQAMTHPSHHLNFGMNPDHARS 873 DR GO; GO:004525; F:ribonuclease III activity; IEA. DR GO; GO:006396; P:RNA processing; IEA. DR InterPro; IPR011597; Ds RNA\_bd. DR InterPro; IPR00999; RNase\_III. DR Pfam; PF00035; drmi; 1. DR Pfam; PF00636; Ribonuclease\_3; 2. DR SMART; SM00358; DSRN; 1. DR SMART; SM00535; RBOC; 2. DR PROSITE; PS50137; DS\_RBD; 1. DR PROSITE; PS00517; RNASE\_3; 1; 2. DR PROSITE; PS50142; RNASE\_3\_2; 2. DR NON\_TER 1 1

Db 917 LSNCGRQPKGDRKQHMHMKKGKQGINTLIMSLRGQDDPTPSRINHNERLEFGDAV 976 DR GO; GO:004525; F:ribonuclease III activity; IEA. DR GO; GO:006396; P:RNA processing; IEA. DR InterPro; IPR011597; Ds RNA\_bd. DR InterPro; IPR00999; RNase\_III. DR Pfam; PF00035; drmi; 1. DR Pfam; PF00636; Ribonuclease\_3; 2. DR SMART; SM00358; DSRN; 1. DR SMART; SM00535; RBOC; 2. DR PROSITE; PS50137; DS\_RBD; 1. DR PROSITE; PS00517; RNASE\_3; 1; 2. DR PROSITE; PS50142; RNASE\_3\_2; 2. DR NON\_TER 1 1

Db 977 EFLTSVHLYYLPSLSEGGGLATYRTAVONOHMLAKKUFLDPENLYAHPDLCRESL 1036 DR GO; GO:004525; F:ribonuclease III activity; IEA. DR GO; GO:006396; P:RNA processing; IEA. DR InterPro; IPR011597; Ds RNA\_bd. DR InterPro; IPR00999; RNase\_III. DR Pfam; PF00035; drmi; 1. DR Pfam; PF00636; Ribonuclease\_3; 2. DR SMART; SM00358; DSRN; 1. DR SMART; SM00535; RBOC; 2. DR PROSITE; PS50137; DS\_RBD; 1. DR PROSITE; PS00517; RNASE\_3; 1; 2. DR PROSITE; PS50142; RNASE\_3\_2; 2. DR NON\_TER 1 1

Db 934 EFLTSVHLYYLPSLSEGGGLATYRTAVONOHMLAKKUFLDPENLYAHPDLCRESL 993 DR GO; GO:004525; F:ribonuclease III activity; IEA. DR GO; GO:006396; P:RNA processing; IEA. DR InterPro; IPR011597; Ds RNA\_bd. DR InterPro; IPR00999; RNase\_III. DR Pfam; PF00035; drmi; 1. DR Pfam; PF00636; Ribonuclease\_3; 2. DR SMART; SM00358; DSRN; 1. DR SMART; SM00535; RBOC; 2. DR PROSITE; PS50137; DS\_RBD; 1. DR PROSITE; PS00517; RNASE\_3; 1; 2. DR PROSITE; PS50142; RNASE\_3\_2; 2. DR NON\_TER 1 1

Db 1037 RHAMANCFEALIG 1049 DR GO; GO:004525; F:ribonuclease III activity; IEA. DR GO; GO:006396; P:RNA processing; IEA. DR InterPro; IPR011597; Ds RNA\_bd. DR InterPro; IPR00999; RNase\_III. DR Pfam; PF00035; drmi; 1. DR Pfam; PF00636; Ribonuclease\_3; 2. DR SMART; SM00358; DSRN; 1. DR SMART; SM00535; RBOC; 2. DR PROSITE; PS50137; DS\_RBD; 1. DR PROSITE; PS00517; RNASE\_3; 1; 2. DR PROSITE; PS50142; RNASE\_3\_2; 2. DR NON\_TER 1 1

Db 994 RHAMANCFEALIG 1006 DR GO; GO:004525; F:ribonuclease III activity; IEA. DR GO; GO:006396; P:RNA processing; IEA. DR InterPro; IPR011597; Ds RNA\_bd. DR InterPro; IPR00999; RNase\_III. DR Pfam; PF00035; drmi; 1. DR Pfam; PF00636; Ribonuclease\_3; 2. DR SMART; SM00358; DSRN; 1. DR SMART; SM00535; RBOC; 2. DR PROSITE; PS50137; DS\_RBD; 1. DR PROSITE; PS00517; RNASE\_3; 1; 2. DR PROSITE; PS50142; RNASE\_3\_2; 2. DR NON\_TER 1 1

RESULT 9

Db Q800US\_MOUSE PRELIMINARY; PRT; 705 AA.

AC Q800US\_

DT 01-JUN-2003 (TREMBL; 24, Created)

DT 01-JUN-2003 (TREMBL; 24, Last sequence update)

DT 01-MAR-2004 (TREMBL; 26, Last annotation update)

DE Rnasen protein (Fragment).

GN Name\_Etch12; Synonyms=Rnasen;

OS Mus musculus (Mouse).

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10050;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=129/Sv x 129/Sv-CP; TISSUE=ES Cell;

RX MEDLINE=22388757; PubMed=12477932; DOI=10.1073/pnas.2426038991;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klaunzer R.D., Collins F.S., Wagner L., Shemesh C.M., Schulz G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Bork P., Jordan H., Moore T., Max S.I., Wang J.J., Haile F.,

RA Diatchenko L., Marusina K., Fammer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Tsohickyi S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullally S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Kulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Rahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimes J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalicka U., Smalius D.E.,

RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.; Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.",

RT proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RL Submitted (APR 2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC050057; AAH50057.1; -; mRNA.

DR HSSC; 067082; 1JFZ.

DR Ensemble; ENSMUSG00000022191; Mus musculus.

DR MGI; MGI:1261425; Etch12.

DR MGI; MGI:1261425; Rnasen.

DR GO; GO:0005622; C:intracellular; IEA.

DR GO; GO:0003725; F:double-stranded RNA binding; IEA.

RESULT 10

Db Q9XNS\_DROME PRELIMINARY; PRT; 1327 AA.

ID Q9XNS\_DROME

AC Q9XNS\_

DT 01-NOV-1999 (TREMBL; 12, Created)

DT 01-NOV-1999 (TREMBL; 12, Last sequence update)

Db 1330 EKYNPFQMMQKRFKRYQKELKMRWREHQEREPEDDIK 1374 DR GO; GO:004525; F:ribonuclease III activity; IEA. DR GO; GO:006396; P:RNA processing; IEA. DR InterPro; IPR011597; Ds RNA\_bd. DR InterPro; IPR00999; RNase\_III. DR Pfam; PF00035; drmi; 1. DR Pfam; PF00636; Ribonuclease\_3; 2. DR SMART; SM00358; DSRN; 1. DR SMART; SM00535; RBOC; 2. DR PROSITE; PS50137; DS\_RBD; 1. DR PROSITE; PS00517; RNASE\_3; 1; 2. DR PROSITE; PS50142; RNASE\_3\_2; 2. DR NON\_TER 1 1

Db 661 EKYNPFQMMQKRFKRYQKELKMRWREHQEREPEDDIK 705 DR GO; GO:004525; F:ribonuclease III activity; IEA. DR GO; GO:006396; P:RNA processing; IEA. DR InterPro; IPR011597; Ds RNA\_bd. DR InterPro; IPR00999; RNase\_III. DR Pfam; PF00035; drmi; 1. DR Pfam; PF00636; Ribonuclease\_3; 2. DR SMART; SM00358; DSRN; 1. DR SMART; SM00535; RBOC; 2. DR PROSITE; PS50137; DS\_RBD; 1. DR PROSITE; PS00517; RNASE\_3; 1; 2. DR PROSITE; PS50142; RNASE\_3\_2; 2. DR NON\_TER 1 1

DT 13-SNP-2005 (TCMBLref\_31, Last annotation update)  
 DE CG8730-PA (LD2003Op) (Ribonuclease).  
 GN Name=droso; ORFNames=CG8730;  
 OS Drosophila melanogaster (fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Brachycera; Muscomorpha;  
 OC Ephydriidae; Drosophilidae; Drosophila.  
 OC NCBI\_TaxID=7227;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides G.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandt R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.I.G.,  
 RA Abril J.F., Abyzov A.A., An H.-J., Andrews-Pflaum C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Baeckman K.Y., Benos P.V., Berman B.P., Blaustein D., Bolshakov S.,  
 RA Borkovska D., Botchan M.R., Boucic J., Brokstein P., Brottier J.,  
 RA Burtis K.C., Buram D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., May A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doupe L.E., Downes M., Dugan-Stocka S., Dunkov B.C., Dunn P.,  
 RA Durbin R.K., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Fosler C., Gabril A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland J., Ibeagwam C.,  
 RA Jalaai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kraitz D., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levittky A.B., Li J.H., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobrery C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclob J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Purii V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.-C., Siden-Kiamios I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svärskas R., Tector C., Turner R., Venter J.E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasbaran D.A., Weissenbach J.,  
 RA Williams S.M., Woodage T., Wolley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Yeh R.-F., Zaveri J.S., Zhan H., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.-H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RA "The genome sequence of *Drosophila melanogaster*,"  
 RT RT melangaster euchromatic genome sequence,"  
 RL Science 287:2185-2195 (2000).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22426065; PubMed=12537568;  
 RA Celniker S.E., Wheeler D.A., Kromiller B., Carlson J.W., Halpern A.,  
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,  
 RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,  
 RA Paclob J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
 RA Svärskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
 RA Weintraub G., Scheerer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,  
 RT RT finishing a whole-genome shotgun: release 3 of the *Drosophila*  
 RT melangaster euchromatic genome sequence,"  
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22426070; PubMed=12537573;  
 RA Kaminker J.S., Bergman C.M., Kromiller B., Carlson J.W., Svärskas R.,  
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Celniker S.E.;  
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin: a genomic perspective,"  
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22426069; PubMed=12537572;

RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,  
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Bernick B.P.,  
 RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,  
 RA Harris N.L., Richter J.J., Russo S., Schroeder A.J., Snu S.Q.,  
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
 RA Lewis S.E.;  
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a systematic review,"  
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RX Berkeley Drosophila Genome Project;  
 RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,  
 RA Hoskins R., Stapleton M., Paclob J., Park S., Svärskas R., Smith E.,  
 RA Yu C., Rubin G.,  
 RT "Drosophila melanogaster release 4 sequence,";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP NUCLEOTIDE SEQUENCE.  
 RX FLYBase;  
 RA Borkovska D., Botchan M.R., Bouch J., Brokstein P., Brottier J.,  
 RA Burtis K.C., Buram D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., May A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doupe L.E., Downes M., Dugan-Stocka S., Dunkov B.C., Dunn P.,  
 RA Durbin R.K., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Fosler C., Gabril A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland J., Ibeagwam C.,  
 RA Jalaai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kraitz D., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levittky A.B., Li J.H., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobrery C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclob J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Purii V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.-C., Siden-Kiamios I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svärskas R., Tector C., Turner R., Venter J.E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasbaran D.A., Weissenbach J.,  
 RA Williams S.M., Woodage T., Wolley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Yeh R.-F., Zaveri J.S., Zhan H., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.-H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RT RT finishing a whole-genome shotgun: release 3 of the *Drosophila*  
 RT melangaster euchromatic genome sequence,"  
 RL Science 287:2185-2195(2000).  
 RN [9]  
 RP NUCLEOTIDE SEQUENCE.  
 RX STRAIN=Berkeley;  
 RA Stapleton M., Carlson J., Chavez C., Frise E., George R., Paclob J.,  
 RA Park S., Wan K., Yu C., Celniker S.,  
 RT Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
 RN [10]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=20179701; PubMed=1073462; DOI=10.1016/S0378-1119(99)00571-5;  
 RA Filippov V., Solovyev V., Filippova M., Gill S.S.,  
 RA Filippov V., Solovyev V., Filippova M., Gill S.S.,  
 RA Park S., Wan K., Yu C., Celniker S.,  
 RT Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
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 DR EMBL; AE03383; AAF9169.1; -; Generic\_DNA.  
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 DR EMBL; BT02353; AAY4903.1; -; mRNA.  
 DR EMBL; AF116572; AAD31170.1; -; mRNA.  
 DR HSSP; O67882; JIFZ.  
 DR INTACT; QXKYN; -.  
 DR Ensemble; CG8730; Drosophila melanogaster.  
 DR FlyBase; FBgn026722; CG8730.  
 DR FlyBase; FBgn026722; drosophila.  
 DR GO; GO:0005622; C:intracellular; F:double-stranded RNA binding; IEA.  
 DR GO; GO:003725; F:ribonuclease III activity; IEA.  
 DR InterPro; IPR001159; DS\_RBD.  
 DR InterPro; IPR000999; RNase\_III.  
 DR pfam; PF00035; dsrm; 1.  
 DR pfam; PF00636; Ribonuclease\_3; 2.  
 DR SMART; SM00358; DSRM; 1.  
 DR SMART; SM00535; RISOC; 2.  
 DR PROSITE; PSS0137; DS\_RBD; 1.  
 DR PROSITE; PSS0517; RNASE\_3\_1; 1.  
 DR PROSITE; PSS05142; RNASE\_3\_2; 2.  
 DR PROSITE; PSS05142; RNASE\_3\_2; 2.  
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Qy 138 QGTFPPMMPSPMPHPPPPVMPQQVNYQVPPG-----SHNFP 179







DR CO; GO:0005622; C: intracellular; IEA.  
 DR GO; GO:0003725; F: double-stranded RNA binding; IEA.  
 DR GO; GO:000519; F: endonuclease activity; IEA.  
 DR GO; GO:0004525; F: ribonuclease III activity; IEA.  
 DR GO; GO:000396; F: RNA processing; IEA.  
 DR InterPro; IPR001159; DS RBD.  
 DR InterPro; IPR000999; RNase\_III.  
 DR PFam; PF00035; d8rm; 1.  
 DR SMART; SM00358; DSRM; 1.  
 DR PROSITE; PS00535; RIBO; 2.  
 DR PROSITE; PS00535; RIBO; 1.  
 DR PROSITE; PS50137; DS RBD; 1.  
 DR PROSITE; PS50142; RNase\_3\_2; 2.  
 DR NON\_TER 836 836 PT; 1.  
 SEQUENCE 836 AA; 96229 MW; 8D3E0BD04953877D CRC64;  
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 DR 1 HHLRHLWDLWYDPGENDGPCCRSCSRSRGGRRGKSKYPGEGFPKCIPISSNNAKLYH 60  
 DR 574 YRITVSPPTNFTLDRPTVIEYDHEYFEGFSMPAHAPLTNIPLCKVTFRNIDYTHFIE 633  
 DR 61 YRITISPPTNFTLFTKPTIKHDOHEFLPEGFSSLAHEPIGELPTCKVTFRNIEYTLIE 120  
 DR 634 EMPENFCVKGELSFSLERLILEYDWNLKGPLEEDSPCCPCPREFMPFRPRFEDG 693  
 DR 121 EMMENFCVKGELSFSLERLILEYDWNLKGPLEEDSPCCPCPREFMPFRPRFEDG 179  
 DR 694 KEVLMSHQIILYLURCSKALVPEEELQYKABECKGMIIVTWTGPKSSVR 753  
 DR 180 KEVLMSHQIILYLURCSKALVPEEELQYKABECKGMIIVTWTGPKSSVR 239  
 DR 754 IDOLDREOFNPDPVITPFTIYHGRPAQSLYQGDPQYOKLWNSYVKURHLLANSPKVQ 813  
 DR 240 VDOLDRNV--GDUPEANAIENG----YAGNPYQKAWREYIKEFHLIANSKPSFE 290  
 DR 814 DQKQKLAQREAAQKIKONTMREYVTELSSQFCWKGIRSPVQHAMMLPVLTHIRY 873  
 DR 291 DRCRKLREAKNRLIEMRNGMCRNNTIAVSAKAFHRTGIMCVOHAMLIPVLTGHFR 350  
 DR 874 QCLMHLDKLGITFQDRCLLQJAMTHSHHILFGMDHARNSLSNGIROPKGDRKH 933  
 DR 351 RSLAVLVRIGTGTPTNRYLQALTHSYKENGTDHARNSLSNGIROPKGDRKH 410  
 DR 934 RHMHRKGKGTINTIMSRGLQDOPTPSPRINRHLERLEFGDAVTFPLTSVHLYLFPSEE 993  
 DR 411 YMNTRKRKGINTIJSIMSRFGKHEHDSNITHNERLEFLGDAVTFPLTSVHLYLFPDDE 470  
 DR 994 GCLATRTAIYONQHMLAKLKEFDPFLYHGPDLCRSDLRHAMNCEPBLIGAVYL 1053  
 DR 471 GCLATRTAIYONQHMLAKLKEFDPFLYHGPDLCRSDLRHAMNCEPBLIGAVYL 530  
 DR 1054 EGSLEBKAQLQFLRFLNPD-LRREVWLNTPHPLQLOBPNTPLQRLIBTSPVQKLTEFEE 1112  
 DR 531 DCGIEVADRVFAVYALQFQEDDTGJGIWNPSPQBLQEPGLRHRHDSFEMKLTREFD 590  
 DR 1113 AIGVIFTHVRLARAFTTFTVFNHLTGHGRNMRERFLGDSIMQVATEYLPFLPHDPHEG 1172  
 DR 591 SIVGOVFNHRLAARAFTRDSICPTNLTIGSNSQRLREFLGDITVQLCISEYLYKHFPHHEG 650  
 DR 1173 HUTLASSLVLNRTQATQVAEGMQEYAI-TDVKTKRPRVGLRTKLADLASSPIALYTD 1231  
 DR 651 HUSLRSLSLVLNRTQAVCDLGMTOAVYVSNPK---ADLTKDORADLSEPLGALYVD 706  
 DR 1232 KULEVYHTFMVCCFPKLFELQDNDPDKSPLQCCLTLT-EGKEPDPLYKLTQV 1290  
 DR 707 KCLYCEMFCHVCLFPRLQDF1MNQDNDPDKSPLQCCLTLT-RTMDGEGPDPVYKVIECT 766

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 DT 10-MAY-2005 (TREMBrel. 30, Last annotation update)  
 DE Nuclear RNase III Drosha variant (Fragment).  
 OS Homo sapiens (human).  
 OC BukaYota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Cetartiodactyla;  
 OC Homo.  
 OR NCBI\_TAXID=9606;  
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 RC TISSUE=Brain;  
 RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,  
 RA Ohara O., Nagase T., Kikuno F.R.,  
 RT "None Title.";  
 RT Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB209501; BAD92738.1; -; mRNA.  
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 SQ 827 KRQ 829

Query Match 30.6%; Score 2298; DB 2; Length 432;  
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 DR 616 PLCKVTFRNIDYTFEEMPENFCVKGELSFSLERLILEYDWNLKGPLEEDSPC 675  
 DR 67 PLCKVTFRNIDYTFEEMPENFCVKGELSFSLERLILEYDWNLKGPLEEDSPC 126  
 DR 676 CPRFHEMPFRVPLDGGKEVLSMHQIILYLURCSKALVPEEELANLQWEEBLEWQKAE 735  
 DR 127 CPRFHEMPFRVPLDGGKEVLSMHQIILYLURCSKALVPEEELANLQWEEBLEWQKAE 186  
 DR 736 ECKGMITVNPCTPKSSVYRIDQDREOFNPDTFPTIVHFGTRPAQSLYADPQYOKLW 795  
 DR 187 ECKGMITVNPCTPKSSVYRIDQDREOFNPDTFPTIVHFGTRPAQSLYADPQYOKLW 246  
 DR 795 SYVKLRLLLANSPKVQKTDOKLQABEALOKRQNTMREYVTELSQDFWKGIRSD 855  
 DR 247 SYVKLRLLLANSPKVQKTDOKLQABEALOKRQNTMREYVTELSQDFWKGIRSD 306  
 DR 856 VQHAMMLPVLTHIRYQCLMHDKLGITFQDRCLLQAMTHPSHHLNFGMNPDHARN 915  
 DR 307 VQHAMMLPVLTHIRYQCLMHDKLGITFQDRCLLQAMTHPSHHLNFGMNPDHARN 366  
 DR 916 SLSNCGTRQPKYGDKRVHMMRKGKGTNTLNIMSRGQDQDPTSPSRINHNTLEFLGDAV 975  
 DR 367 SLSNCGTRQPKYGDKRVHMMRKGKGTNTLNIMSRGQDQDPTSPSRINHNTLEFLGDAV 426  
 DR 976 VEPFLT 980  
 DR 427 VEPFLT 431

Search completed: February 3, 2006, 19:41:12  
 Job time : 297 sec



GenCore version 5.1.7  
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Om protein - protein search, using sw model

Run on: February 3, 2006, 19:41:24 ; Search time 56 Seconds  
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2028.507 Million cell updates/sec

Title: US-10-079-185-2

Perfect score: 7500

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 83675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing First 45 summaries

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2: /cgn2.6/ptodata/1/iaa/6\_COMB.pop: \*  
3: /cgn2.6/ptodata/1/iaa/H\_COMB.pop: \*  
4: /cgn2.6/ptodata/1/iaa/PCTNS\_COMB.pop: \*  
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Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and 18 is derived by analysis of the total score distribution.

### SUMMARIES

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2	2463	32.8	466	2 US-09-900-425B-37
3	890	11.9	412	2 US-09-900-425B-3
4	496	6.6	115	2 US-09-513-99C-4635
5	316	4.2	553	2 US-09-949-016-7961
6	312.5	4.2	241	2 US-09-107-53A-5434
7	284.5	3.8	232	2 US-09-583-110-4554
8	284.5	3.8	232	2 US-09-107-433-4394
9	284.5	3.8	998	2 US-09-949-016-7757
10	277.5	3.7	232	1 US-09-899-674-2
11	277.5	3.7	232	2 US-09-213-010-2
12	277.5	3.7	232	2 US-09-213-011-2
13	271.5	3.6	386	2 US-09-461-774-10
14	267	3.6	243	2 US-09-945-087-2
15	264.5	3.5	1404	2 US-08-801-308-1
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17	262	3.5	226	2 US-09-900-425B-6
18	262	3.5	971	2 US-09-248-79A-19331
19	260.5	3.5	245	2 US-09-710-279-1658
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22	252	3.4	228	2 US-09-543-68A-7646
23	248.5	3.3	904	2 US-09-516-59A-615
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25	239.5	3.2	865	2 US-09-81-76B-19
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27	239.5	3.2	865	2 US-09-957-99A-19

### ALIGNMENTS

RESULT 1  
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Sequence 2, Application US/09900425B  
; Patent No. 673512  
; GENERAL INFORMATION:  
; APPLICANT: Crooke, Stanley T.  
; WU, Hongjiang  
; TITLE OF INVENTION: Human RNase III And Compositions And Uses Thereof  
; FILE REFERENCE: ISS5029/ISPR-0522  
; CURRENT APPLICATION: US/09/900, 425B  
; CURRENT FILING DATE: 2001-07-06  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO: 2  
; LENGTH: 1374  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-900-425B-2

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Matches 1374; Conservative 0; Pairs 0; Gaps 0;

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DQ 361 KQARWEERDRSDNQSGKDQYTSIKEKESEBTMDKNEEEELKPKWIRCHSEN 420

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 Db 421 YSSDDPMQVGSTVGTSLRDLYKFEELGSROEKAKARPPWEPKTKLDEDLESS 480  
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 ; Parent No. 6737512  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wu, Hongjiang  
 ; TITLE OF INVENTION: Human RNase III And Compositions And Uses Thereof  
 ; FILE REFERENCE: US15029/15PH-0522  
 ; CURRENT APPLICATION NUMBER: US/09/900,425B  
 ; CURRENT FILING DATE: 2001-07-06  
 ; NUMBER OF SEQ ID NOS: 37  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 3  
 ; LENGTH: 412  
 ; TYPE: PRT  
 ; ORGANISM: Caenorhabditis elegans  
 US-09-900-425B-3

Query Match

11.9%; Score 890; DB 2; Length 412;

Best Local Similarity 43.1%; Pred. No. 1.4e-61;

Matches 181; Conservative 85; Mismatches 136; Indels 18; Gaps 7;

; APPLICANT: Wu, Hongjiang

; APPLICANT: Crooke, Stanley T.

US-09-900-425B

; Sequence 37, Application US/09900425B

; Parent No. 6737512

; GENERAL INFORMATION:

; APPLICANT: Wu, Hongjiang

; APPLICANT: Crooke, Stanley T.

; APPLICANT: Crooke, Stanley T.

QY 944 TLINMSRLGQDPTPSRINHNERLEPLGDAVFLTSYHLYLFLPSLEGGATYRTI 1003

RESULT 5

2 SLFNIMKGTSGGEP---IHNRRRLYBLGDAVELVSHHVFMLTHFEGSLATRTAL 57

Db 1004 VONOHMLAKKLESDPFLMLYAHGPDLCRESDIRHMANCETALIGAVYLGSLEAKQL 1063

Qy 58 VONRMLATLAKNCRDEMLOVSHGADLNVAEFAVMAIYLDGGLAPCDVI 117

Db 1064 FGRILF-NPDLDREWMLNPLHPLQLOEPNTDROLIBETSPVQLKLTPEEAGVIFHVR 1122

Qy 118 FSKANGYQHOPVKEKWDHNEHLLRKEPDQCDRDRSITPMLTSHALEERIGQFENR 177

Db 1123 LLARAFTRLTGVFNHILTGHNORMERFLGDSIMOLAVATEYLTHPDHGEHTLTLASSLV 1182

Qy 178 LLAKAFTRRNIPNNDLTKGHNQRLNGLGDSVFLQLTIVSDFLYRPFTHEGMNLRTSLV 237

Qy 1183 NNRTQPAKVAELBGMOBEAINTDKTRPV--GLRTKLADLESIAALYTDKDELYVHT 1239

Db 238 SNOTQAVVCDIDGPFV-----KAPYKPEBLKDKADIAVEAFGALYDGRIGHCRCA 292

Qy 1240 FMNVGFFPRKLEFIINQDWDNPKSQILOQCCFLTR-TEGKEDPDLVYKLTQTVGSHARTY 1298

Db 293 FIRIVFCPRUKHFISEKWDKASHQOWCLAMRDSSEDFMDPEVRLGIEGPTNRP 352

Qy 1299 TAVYFKGERIGCGKPSIQCQEMA---AMDALEKONPOM-AHQKRFGRKVRBLIKE 1354

Db 353 KIAVYKKGKRLASAESNVHKAELVAAELANLESMSFSKMKAKONSNRRLEODTSD 412

RESULT 4

US-09-513-999C-4635

Qy ; Sequence 4635, Application US/09513999C

Db ; Patent No. 6783961

Qy ; GENERAL INFORMATION:

Db ; APPLICANT: Dumas Milne Edwards, J.B.

Qy ; APPLICANT: Duciert, A.

Db ; APPLICANT: Gloriano, J.Y.

Qy ; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

Db ; Patent No. 6783961

Qy ; FILE REFERENCE: 59, US2, REG

Db ; CURRENT APPLICATION NUMBER: US/09/513, 999C

Db ; CURRENT FILING DATE: 2000-02-24

Qy ; PRIOR APPLICATION NUMBER: US 60/122, 487

Db ; NUMBER OF SEQ ID NOS: 36601

Qy ; SOFTWARE: Patent.pm

Db ; SEQ ID NO 4635

Qy ; LENGTH: 115

Db ; TYPE: PRT

Qy ; ORGANISM: Homo sapiens

Db ; FEATURE: SIGNAL

Qy ; LOCATION: -23,-1

Db ; OTHER INFORMATION: score 5.9

Qy ; OTHER INFORMATION: seq TIRFLTLQSKNA/KR

Db ; NAME/KEY: UNSURE

Qy ; LOCATION: 3

Db ; OTHER INFORMATION: xaa=Ala or Pro

Qy ; OTHER INFORMATION: US-09-513-999C-4635

Query Match 6 6%: Score 496; DB 2; Length 115;

Best Local Similarity 95.7%; Pred. No. 2.2e-31; 2; Indels 0; Gaps 0;

Matches 88; Conservative 2; Mismatches 0; Gaps 0;

Db 511 KKAHDPLRHLDELWIDPGQMDGPKCSAKARRGIGRHSIVPGEEAIKPCPRMTNNAGR 570

Qy 24 KRXNDLRLHSLWYDQGQMDGPKCSAKARRGIGRHSIVPGEEAIKPCPRMTNNAGR 83

Db 571 LFHVRITVSPPTNFFLDRPTVIEYDHEYTFE 602

Qy 84 LFHVRITVSPPTNFFLDRPTVIEYDHEYTFE 115

RESULT 6

US-09-107-532A-5434

Qy ; Sequence 5434, Application US/09107532A

Db ; Patent No. 6583275

Qy ; GENERAL INFORMATION:

Db ; APPLICANT: Lynn A Doucette-Stamm and David Bush

Qy ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

Db ; NUMBER OF SEQUENCES: 7310

Qy ; CORRESPONDENCE ADDRESS:

Db ; ADDRESSEE: GENOME THERAPEUTICS CORPORATION

Db ; STREET: 100 Beaver Street

Db ; CITY: Waltham

ZIP: 02354  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: CD/ROM ISO9660  
 COMPUTER: PC  
 OPERATING SYSTEM: <Unknown>  
 SOFTWARE: ASCII

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/107,532A  
 FILING DATE: 30-Jun-1998  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 60/085,598  
 FILING DATE: 14 May 1998  
 APPLICATION NUMBER: 60/051571  
 FILING DATE: July 2, 1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Arinello, Pamela Deneka  
 REGISTRATION NUMBER: 40,489  
 REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (781)893-5007  
 TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 5434:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 241 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: YES

ORIGINAL SOURCE:  
 ORGANISM: Enterococcus faecium

FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: (B) LOCATION 1..241  
 SEQUENCE DESCRIPTION: SEQ ID NO: 5434;

US-09-107-532A-5434

Query Match Best Local Similarity 33.5%; Score 312.5; DB 2; Length 241; Matches 77; Conservative 50; Mismatches 90; Indels 13; Gaps 7;

Qy 1105 QRLTEFPEBAIGVTFVRLRLLAFTLTVGFH--LTLGHNORMELGDSIMOLVATEYL 1162  
 Db 17 QRLTKEKVNNTVFDLNLLEQFTHSYVNRHNLQSDNRLEPLGDAVLELMVSQL 76  
 Qy 1163 PIRHPDHHEGHTILRSLSVNRTOQAVAEGLGMQEYAITNDKTKPVGRLTK-TLADL 1220  
 Db 77 FRLYFPLPEGKLT-KTRAIVREDSLSKPAFKSCHFDQYPLLG-KGEENSGGTRPALLCDL 135  
 Qy 1221 LEPFIAALYTDKOLEYHTFMNCFFPLKEFTLNGQWNDPSQLOQCLTIRTEKEPD 1280  
 Db 136 FERFLGALYDQGFDTHAFIEKVIFPKVKGAFSHM-DIKTKLQB--VHQSG--D 1188  
 Qy 1281 IPL-YKLUQTVPSHARTTYTVAVYFKGERIGGKGKPSIQOANGAAMDAL 1329  
 Db 189 VSIERYLINEEGPAHERVFWIEVYDDQDILGQGSKSKLARQAENAL 238

RESULT 8  
 US-09-107-433-4394  
 Sequence 4394 Application US/09107433  
 Patent No. 6000744  
 GENERAL INFORMATION:  
 APPLICANT: Lynn A Doucette-Stamm and David Bush  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTIC PURPOSES

NUMBER OF SEQUENCES: 5206  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
 STREET: 100 Beaver Street  
 CITY: Waltham  
 STATE: Massachusetts  
 ZIP: 02354  
 COMPUTER READABLE FORM:  
 COMPUTER: <Unknown>  
 MEDIUM TYPE: CD/ROM ISO9660  
 OPERATING SYSTEM: <Unknown>  
 SOFTWARE: <Unknown>

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/107,433  
 FILING DATE: 30-Jun-1998  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Arinello, Pamela Deneka  
 REGISTRATION NUMBER: 40,489  
 REFERENCE/DOCKET NUMBER: GTC-011

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (781)893-5007  
 TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 4394:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 235 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: YES

RESULT 7  
 US-09-583-110-4554  
 Sequence 4554 Application US/09593110  
 GENERAL INFORMATION:  
 APPLICANT: Lynn Doucette-Stamm et al.  
 TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus  
 FILE REFERENCE: PATH0-07A  
 CURRENT APPLICATION NUMBER: US/09/583,110  
 CURRENT FILING DATE: 2000-05-26  
 PRIOR APPLICATION NUMBER: US 09/107,433  
 PRIOR FILING DATE: 1998-06-30  
 PRIOR APPLICATION NUMBER: US 60/085,131  
 PRIOR FILING DATE: 1998-05-12  
 PRIOR APPLICATION NUMBER: US 60/051,553

US-09-583-110-4554

Query Match Best Local Similarity 32.9%; Score 284.5; DB 2; Length 232; Matches 76; Conservative 48; Mismatches 90; Indels 17; Gaps 8;

Qy 1108 TEPEEAIGVFTHVRLRLLAFTLTVGFH--LTLGHNORMELGDSIMOLVATEYLH 1165  
 Db 6 TVLKQHFAIETDKULLETFHTHSYANERLKLKSHNRLFQDAVLLQILSVELYKK 65  
 Qy 1166 FPDHHEGHTILRSLSVNRTOQAVAEGLGMQEYAITNDKTKPVGRLTK--TLADLLES 1223  
 Db 66 YPKKPEGDSKURAMIVREESLAGFARDQDFQ-1IKLGKBEKSGGRNQDFTLGAPEA 124  
 1224 FIAALYTDKOLEYHTFMNCFFPLK-EPILQDMDNPKSQLQCCLTURTEKEPD 1281  
 Db 125 FGLALLQDQVAKVQFPIQWIPKVEAGEREMITYD--KTHLQB--LHQVW--DV 175  
 Qy 1282 PL-YKLUQTVPSHARTTYTVAVYFKGERIGGKGKPSIQOANGAAMDAL 1331  
 Db 176 AIRYQVISETOGPADKVFVDPDVLFVLECKSICQGQGSKKLAQEANKNAVK 226

RESULT 8  
 US-09-107-433-4394  
 Sequence 4394 Application US/09107433  
 Patent No. 6000744  
 GENERAL INFORMATION:  
 APPLICANT: Lynn A Doucette-Stamm and David Bush  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTIC PURPOSES

NUMBER OF SEQUENCES: 5206  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
 STREET: 100 Beaver Street  
 CITY: Waltham  
 STATE: Massachusetts  
 ZIP: 02354  
 COMPUTER READABLE FORM:  
 COMPUTER: <Unknown>  
 MEDIUM TYPE: CD/ROM ISO9660  
 OPERATING SYSTEM: <Unknown>  
 SOFTWARE: <Unknown>

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/107,433  
 FILING DATE: 30-Jun-1998  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Arinello, Pamela Deneka  
 REGISTRATION NUMBER: 40,489  
 REFERENCE/DOCKET NUMBER: GTC-011

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (781)893-5007  
 TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 4394:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 235 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: YES

## ORIGINAL SOURCE:

ORGANISM: *Streptococcus pneumoniae*

## FEATURE:

NAME/KEY: misc\_feature

## LOCATION: (B) LOCATION 1.. 236

## SEQUENCE DESCRIPTION: SEQ ID NO: 4394:

US-09-107-433-4394

Query Match 3.8%; Score 284.5; DB 2; Length 236;

Best Local Similarity 32.9%; Ped. No. 2.8e-14;

Matches 76; Conservative 48; Mismatches 90; Indels 17; Gaps 8;

Oy 1108 TFRBEATGVIFVHVRLLARAFPLRTVGFNH-LTGLGNQRMEPLGDSIMQVALATEVLFH 1165

Db 10 TWLKLNHFAIEPTDKKLUETTAFTHTSYANERHLRKLISHNERLFLGDAVOLIISYLYKK 69

Oy 1166 FPDHHEGHLTLRSSLVNNRTOAKVABEGLMGMOBYAITNDKTRPVGRTK-TLADLLES 1223

Db 70 YPKKPGEDLSKURAMITREESLAGFARDQFDFP-IKLGKSEKSGGRRNRTGILGAFE 128

Oy 1224 PIAALYTDKDLB1VHTFMNCVCPPLR--EFTLNQMDPKSOLQOCCLTRTEGKEPDI 1281

Db 129 FIGALLILDKDVKVKEPIYQWVLPKVEAGEFFMITY--KHLQB--LILQVNG--DV 179

Oy 1282 PI-YKTLQTVGSHARTVYAVTFKGGRIGCGKGPSIQQAENGAADEK 1331

Db 180 AIRYQVISETGAHDVKVDFDEVLEVGSKSICGQGRSKKLABEAKNAVEK 230

RESULT 9  
US-09-949-016-7757

; Sequence 7757, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: C1001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows version 4.0

; SEQ ID NO 7757

; LENGTH: 998

; TYPE: PRT

; ORGANISM: Human

; US-09-949-016-7757

Query Match 3.8%; Score 284.5; DB 2; Length 998;

Best Local Similarity 22.7%; Ped. No. 2.3e-13;

Matches 151; Conservative 63; Mismatches 206; Indels 245; Gaps 30;

Oy 27 ARPSA-PSFRQNLRLHPOQQPVQYEPSSA-----PSTTFNSNAPNPLPPR 75

Db 350 ARGGGGPGWERSN-KIGYLVSPQQIRGGRSCYRSINRGHHSERSQRTGGS-LPAT 407

Oy 76 PRPVPPPPMPPPSAQGQLLPPC1IRPPFHNQHMRHPPVPPCPMPMPMPMPCHNNPPVGA 135

Db 408 PVFVPPVPP-----PLVPPPP-----HTPLPL--PGVPPQFSPQFP--PGQ 445

Oy 136 PRGQGTTPPMMPPSMMPHPPPPVMPQDQN-----YQYPP----- 170

Db 446 PPAG--YSVPPPGF-PAPANLSTPWVSSVQTAHSNTIPTQAPPLSREFYRBQR 501

Oy 171 -----GYSHEWPPPSFNS 184

Db 502 LK3EEKUKSKLDFTFNDAKEJMEKKQKERRRSRSRSKSPYSGSSYSSRSSTYTKRS 561

Oy 185 FQNNPSSFLPSANNSPPFRHLPPVPLKAPSERRSRPERLKYDDHRHRSNGCERH 244

Db 562 GSTRRSYSRSRSRSRSRSYSRSPP-----RGRGKSNY--RSRSRSHG--YH 608

Oy 245 RSLDRRSRGRSPDRRDRSRYSDYD-RGRTSPRSRSYERER----- 289

Db 609 RS-----RSRSPPYRYSRSRSRSPQFRGQSPNKRNVPPGTEREFNRYREVPPYDMK 663

Oy 290 -----ERHRDRNRSPLERSYKEYRSGRSGLSSVPEPAGCTPELPG 336

Db 664 AYGRSVDPRDPPEKEYRE-----WERKPREWYCYKGAGQPRPSA----- 709

Oy 337 IKNNTSWAP----PLIVNHRSPSREKKRARWEEKRDRWSNDNQSG----- KD 381

Db 710 --NRNENSPERFLPLAUN--SPFTRGRSREUDYVGOSHSRNSNTGSPKLSARDQHNO 764

Oy 382 KNTSKIKEKEPRETMPD-----KNEBEERELLKPVWRCTH-----SENY 421

Db 765 KONTSKIKEKESENAPGDKGKNGKHKRRKGEESEOFNPLLETSRSRBPTEVNEK 824

Oy 422 YSS-----DPMQVQGSTWVGSRLADLYDFEEEL-----GSRQ 456

Db 825 TDSLFVPLRSRDDATPVDEMD--AISTFKVSSEKDREROKPKAKGDKTRKRNQGSAV 882

Oy 457 EKKAARPPWEPPTKUDDELESSESSEC-----BSEDESTCSSSDSEVFDTAELK 509

Db 883 SKKENITWPKAQPQEQKVDGERERSRSPSEPPIKAKBETPKTNTKSSSQQDKEKITGTP 942

Oy 510 RKKAH 514

Db 943 R-KAH 946

RESULT 10  
US-08-869-674-2

Sequence 2, Application US/08869674

; Patent No. 5866365

; GENERAL INFORMATION:

; APPLICANT: Lometto, Michael A.

; APPLICANT: Robenberg, Martin

; TITLE OF INVENTION: NOVEL COMPOUNDS

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dechert, Price &amp; Rhoads

; STREET: 997 Lenox Drive, Building 3, Suite 210

; CITY: Lawrenceville

; STATE: NJ

; COUNTRY: USA

; ZIP: 08843

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA: US/08/869,674

; APPLICATION NUMBER: US/08/869,674

; FILING DATE:

; CLASSIFICATION: 436

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Bloom, Allen

; REGISTRATION NUMBER: 29,135

; REFERENCE/DOCKET NUMBER: GM10013

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 609-520-3214

; TELEFAX: 609-520-3259

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 232 amino acids

TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-869-674-2

Query Match 3.7%; Score 277.5; DB 1; Length 232; Qy 1108 TEPEEAIGVIFTHVRLARAKRAFTLRTVGFNH--LTGHNORMEFLGDSIMOLVATEYLFIH 1165  
 Best Local Similarity 32.5%; Pred. No. 9.8e-14; Mismatches 92; Indels 17; Gaps 8; Matches 75; Conservative 47; Mismatches 92; Indels 17; Gaps 8; Topology: linear

Qy 1108 TEPEEAIGVIFTHVRLARAKRAFTLRTVGFNH--LTGHNORMEFLGDSIMOLVATEYLFIH 1165  
 Db 6 TVLKHNFAIEPADKNULETARTHISYANERHLKISHNERLEFLGDAVLQOLISELYKK 65

Qy 1166 FPDHHRGHTLRLSSLYNNRTOAKVAEELGMQEVYITNDKTRPKRPGVLRK--TLADDLES 1223  
 Db 66 YPKKPEGDLSKLRAMIVREESLAGFARDQFQDF-IKLGKBEKSGGRNRTILGDAFEA 124

Qy 1224 FIAALYDVKOLEYVHTMNCFFPRLK--EFLNQDANDPKSQLQOCCLTRTEGKEPD 1281  
 Db 176 AIRYQVISETGPAHDKFDEVTLVEGKSIGOGQGRSKKLAQOEAKNAVEK 226

RESULT 11  
 US-09-213-010-2  
 ; Sequence 2, Application US/09213010  
 ; Patent No. 6251630  
 GENERAL INFORMATION:  
 APPLICANT: Loretto, Michael A.  
 APPLICANT: Rosenberg, Martin  
 TITLE OF INVENTION: NOVEL COMPOUNDS  
 NUMBER OF SEQUENCES: 4  
 CORRESPONDENCE ADDRESS:  
 ADDRESSE: Dechert Price & Rhoads  
 STREET: 997 Lenox Drive, Building 3, Suite 210  
 CITY: Lawrenceville  
 STATE: NJ  
 COUNTRY: USA  
 ZIP: 08543  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/213,010  
 FILING DATE:  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/869,674  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Bloom, Allen  
 REGISTRATION NUMBER: 29,135  
 REFERENCE/DOCKET NUMBER: GM10013  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 609-520-3214  
 TELEFAX: 609-520-3259  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 232 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-09-213-011-2

Query Match 3.7%; Score 277.5; DB 2; Length 232; Qy 1108 TEPEEAIGVIFTHVRLARAKRAFTLRTVGFNH--LTGHNORMEFLGDSIMOLVATEYLFIH 1165  
 Best Local Similarity 32.5%; Pred. No. 9.8e-14; Mismatches 92; Indels 17; Gaps 8; Matches 75; Conservative 47; Mismatches 92; Indels 17; Gaps 8; Topology: linear

Qy 1108 TEPEEAIGVIFTHVRLARAKRAFTLRTVGFNH--LTGHNORMEFLGDSIMOLVATEYLFIH 1165  
 Db 6 TVLKHNFAIEPADKNULETARTHISYANERHLKISHNERLEFLGDAVLQOLISELYKK 65

Qy 1224 FIAALYDVKOLEYVHTMNCFFPRLK--EFLNQDANDPKSQLQOCCLTRTEGKEPD 1281  
 Db 176 AIRYQVISETGPAHDKFDEVTLVEGKSIGOGQGRSKKLAQOEAKNAVEK 226

RESULT 12  
 US-09-213-011-2  
 ; Sequence 2, Application US/09213011  
 ; Patent No. 6244208  
 GENERAL INFORMATION:  
 APPLICANT: Loretto, Michael A.  
 APPLICANT: Rosenberg, Martin  
 TITLE OF INVENTION: NOVEL COMPOUNDS  
 NUMBER OF SEQUENCES: 4  
 CORRESPONDENCE ADDRESS:  
 ADDRESSE: Dechert Price & Rhoads  
 STREET: 997 Lenox Drive, Building 3, Suite 210  
 CITY: Lawrenceville  
 STATE: NJ  
 COUNTRY: USA  
 ZIP: 08543  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/213,011  
 FILING DATE:  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/869,674  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Bloom, Allen  
 REGISTRATION NUMBER: 29,135  
 REFERENCE/DOCKET NUMBER: GM10013  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 609-520-3214  
 TELEFAX: 609-520-3259  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 232 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-09-213-011-2

Query Match 3.7%; Score 277.5; DB 2; Length 232; Qy 1108 TEPEEAIGVIFTHVRLARAKRAFTLRTVGFNH--LTGHNORMEFLGDSIMOLVATEYLFIH 1165  
 Best Local Similarity 32.5%; Pred. No. 9.8e-14; Mismatches 92; Indels 17; Gaps 8; Matches 75; Conservative 47; Mismatches 92; Indels 17; Gaps 8; Topology: linear

Qy 1108 TEPEEAIGVIFTHVRLARAKRAFTLRTVGFNH--LTGHNORMEFLGDSIMOLVATEYLFIH 1165  
 Db 6 TVLKHNFAIEPADKNULETARTHISYANERHLKISHNERLEFLGDAVLQOLISELYKK 65

Qy 1166 FPDHHRGHTLRLSSLYNNRTOAKVAEELGMQEVYITNDKTRPKRPGVLRK--TLADDLES 1223  
 Db 66 YPKKPEGDLSKLRAMIVREESLAGFARDQFQDF-IKLGKBEKSGGRNRTILGDAFEA 124

QY 1224 PIAALYTDKOLEYVHTPMNCFFPRLK--EFTILNQDNDPKSOLQOCCLTURTEGKEPDI 1281

Db 125 PFLGALLUDKDVAKVKEFPIQYQNMIPKEAGEFEMITDY--KHLQD--LQVNG--DV 175

QY 1282 PLI-YKTLQTVGFSHARRYTYVAVYFKGERIGCGKGSPTQAEQMGAA 1331

Db 176 AIRYQVSETGPAHDKVDFVELVEGKSIGQCGRSKKLARQBAKNAVEK 226

RESULT 13

US-08-461-774-10

; Sequence 10, Application US/09461774

; Patent No. 6087481

; GENERAL INFORMATION:

; APPLICANT: CHAN, Lily

; APPLICANT: CHUNG, Maxey Ching Ming

; APPLICANT: LIM, Renee May Hong

; TITLE OF INVENTION: Bacterial-derived molecules and therapeutic and

; TITLE OF INVENTION: diagnostic uses therefor

; FILE REFERENCE: 1781-0180P

; CURRENT APPLICATION NUMBER: US/09/461,774

; CURRENT FILING DATE: 1999-12-15

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: Patentin ver. 2.1

; SEQ ID NO 10

; LENGTH: 386

; TYPE: PRT

; ORGANISM: Mycobacterium tuberculosis

; US-08-461-774-10

Query Match 3.6%; Score 271.5; DB 2; Length 386; Best Local Similarity 35.4%; Pred. No. 6 1e-13; Matches 80; Conservative 9; Mismatches 88; Indels 49; Gaps 11;

Qy 14 PGRGCPRGRGGHARGAPSAPSFFHQNLRLHPOQQPVQYQYRPSARSTRS----- 64

Db 99 PESGAPR-----PVAVPPMPAPAKM--PAPPA----PAPPSPPTSWLAIVPPV 145

Qy 65 --NSNAPNFLPRPRDPVPPPPMPAAGPPIPPCPRPRPPFENQMHPPPVPPCPFPPMPP 122

Db 146 PPVPPVPPVVKMPPSPVPPVPPVPP--ETPNPPAPPPLENS-----PPVPPVPP 196

Qy 123 PRPCPNPPVQAPPGCT--PPFMPM---PPSMPPPPPMQOVNQYPPGYSHHN 176

Db 197 VPLTLPVPPVPPAPANTSISPLRPAPPBLPKGCPPPMPAPNSPAAPP----S 251

Qy 177 FPPPSFNSFQNNPSSFLPSANNNSSSPFRHLPPYPLPKAPSRRSP 222

Db 252 PPSPPPVVFPTPGPPAPPEPNSSPP---APPAP-PAAPLEGPSP 292

RESULT 14

US-08-965-087-2

; Sequence 2, Application US/08965087

; Patent No. 6346393

; GENERAL INFORMATION:

; APPLICANT: Fedon, Jason C.

; APPLICANT: Loretto, Michael A.

; APPLICANT: Marra, Andrea

; APPLICANT: Palmer, Leslie M.

; APPLICANT: Rosenberg, Martin

; APPLICANT: Warren, Richard L.

; TITLE OF INVENTION: NOVEL RNAs

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSE: Dechert Price &amp; Rhoads

; STREET: 4000 Bell Atlantic Tower, 1717 Arch Stree

; CITY: Philadelphia

; STATE: PA

; COUNTRY: US

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Disquette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: PATSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/965,087

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Dickinson, Todd Q

; REGISTRATION NUMBER: 28,354

; REFERENCE/DOCKET NUMBER: GM10116

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 215-994-2252

; TELEFAX: 215-994-2222

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 243 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-08-965-087-2

Query Match 3.6%; Score 267; DB 2; Length 243; Best Local Similarity 30.5%; Pred. No. 7e-13; Matches 75; Conservative 55; Mismatches 92; Indels 24; Gaps 9;

Qy 1092 NTDRQLETTSPVLUQKLTSEEEAIGVIFTVHLLRAFTLRTV--GENHLTIGHNORMEFL 1149

Db 111 NRFRKFEDT-----KOTNE---LGFTYQNTIQLQDQAFPSHSSFINDEPNMRDHNRLERLEFL 61

Qy 1150 GDSIMQVATEYFLIRPDRHGHLTILRSSLVNNNTQAKVABEGLGQMEVATNDKTKRP 1209

Db 62 GDAVILSVTSRVLFDKHPNLPEGNLTKORATIVCFSVLFANKGLNEMILLG-KGEEK 120

Qy 1210 VGLRTK--TLDLSEPLSIAALYTDKOLEYVHTPMVNCFFPRLIKEFTLNQDN--DPKSQ 1265

Db 1211 TGGTRTSLISDAEFAFPIGALYDQGIDTIVWKAFAEKVIFPVEQ--NELLGVDEKTFQ 177

Qy 1266 QOCCLTURTEGKEPDIPLYKLTQVFSHARRYTYVAVYFKGERIGCGKGSPTQAEQMGAA 1325

Db 178 QBYV---HQDNKGDV-TYNIKEGSPAHRLFTSEVILQCEAIAEGKGKTKKESQRA 232

Qy 1326 MDALEK 1331

Db 233 ESYAQQ 238

RESULT 15

US-08-801-308-1

; Sequence 1, Application US/08801308

; Patent No. 6368790

; GENERAL INFORMATION:

; APPLICANT: Scott, Robert E.

; TITLE OF INVENTION: CDNA ENCODING P2P PROTEINS AND USE OF

; P2P CDNA-DERIVED ANTIBODIES AND ANTISENSE REAGENTS IN

; TITLE OF INVENTION: DETERMINING THE PROLIFERATIVE POTENTIAL OF NORMAL,

; ABNORMAL AND CANCER CELLS IN ANIMALS AND HUMANS

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSE: Weiser &amp; Associates, P.C.

; STREET: 230 S. Fifteenth Street, Suite 500

; CITY: Philadelphia

; STATE: PA

; COUNTRY: USA

; ZIP: 19102

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.  
CURRENT APPLICATION NUMBER: US/08/801,308  
FILED DATE: 18-FEB-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Weiser, Gerard J.  
REGISTRATION NUMBER: 19,763  
REFERENCE/DOCKET NUMBER: 372.6435P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-875-8383  
TELEFAX: 215-875-8394  
INFORMATION FOR SSO ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1404 amino acid  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-801-308-1

QY	942	SVVKD-----FESSSM-----	VIEBDHBYIFQGFSMWAHAPLNPINPLUCKVIRFNIDYTHEBEMMENFCYKGLEFLSL 650
QY	651	FLFR---DILELYDWMUKGPLFEDSPPCPRFFMMPRFVRFLPDCGKEV-----	696
Db	966	SPRKMKMGEVDVEKLERTEBKDKTIASTTPA-----KKIKUNRETCKKIGNAENASTK 1017	
QY	697	-----LSMHQILLYLRL-----CSKALV-----	
Db	1018	EPSBKLESTSSKIKQEKVKGAKAKRKVAGSEGSSSTLVDYTSSTSGLSPVRKSEEKDTK 1077	
QY	715	-----BEEIANMLQ-----WEELENQKYAERCK-----GMIV 742	
Db	1078	RTVIKTMVEYNNNTAARADVTIMIYPOQSKNDIIDESEEDDVKTQPIOSVGKSSII 1137	
QY	743	TNGTKKSSVSR1DQLDIBQFNPDVITFP1IVHGRPAQLSYAGDPQYOKLWK-----SVVKL 800	
Db	1138	KNTTKEPSAT-AKVTKESEQPB-----KLOKUFKEASHELM 1173	
QY	801	RHTI-----ANSPKUKOTDKTIAOREALOKTROONTMRREVTE-LSSGFWKT 850	

Query Match	Best Local Similarity	Score	DB	Length	Indels	Gaps	Matches
Qy	25 HGARPSA--PSFRPQNLLHPCQOPPVQYEPSSA-----	19.9%	Pred.	No	1.4e-11	DB 2;	Length 1404;
Db	314 NAARPGGGRPGMHSN-KLGVLVSPQOIRGRGERSCYRSINRGRHHSRSORTQSPS-LP						Matches 214; Conservative 125; Mismatches 327; Indexes 411; Gaps 50;
Qy	74 PRDPFVPPPPMPSAQSGPLPCCPRIRPPPNNHQMRRHPPVCPFPMPMPPMCPNPNPVP	3.5%					
Db	372 KTCPFVPPVPP-----						
Qy	134 GAPPGQGT--FPPMMPSSMMPHPPPPMPQQNYQ--YPPGY--SHNFPPS-----						
Db	397 GVPFPQSPQFQPSQPPNGYSPPGFPAPANISTACFSPGCVTAHSNTMFTQAPLL						
Qy	182 ---FNSFQNNP-----SSFLPQRANNS-----SPFHFRH---LPPY	2.1%					
Db	457 SREEFYREONDKGREGSKFPYSGSSYSSRSYTDQGLAQHIAHALTSLPSAHTLIDLHD						
Qy	211 PUPKAPSRSPERLKHDDHRDHSHGRGERHRSURRERERSRDRRQSRYSYD						
Db	517 PHPEPEABRS-AMIVHMDLMIDIA-----RSRSPYRYSRSRSRSPPE						
Qy	271 -RGRTPSHRSYERSRER-----						
Db	562 FQGQSPTRGNVPRBEEKERYFNRKYEVPPYDIAKXYGRSVDRDPFKEVRYE-----						
Qy	303 LERSYKKYKRSGRSGYGLSVVPEPAGCTPBLPGEBIKNTDSWAP---PLETVNHRSPSR	1.8%					
Db	616 WERKRYEWYKYYKGYAVGAQPRPSA-----NREDFSPERLILPLNIRN--SPPT						
Qy	359 EKRRARWEEKDRWSN-----QSSGKDKUNVYISIKEKEPEEMPD-----	3.9%					
Db	663 RGRREDYAGQSHRNRLGGNYPBKLSRDRDHNAKDNPKSKEKESENYPGDKGNKHKG						
Qy	399 --KNE---BEEBLIKPWI---RC-----TSENYY---SSPMDQVQDSTVG	4.3%					
Db	723 RKRRENEKEESESSFLNBELLETSSRKCRGSSGIDETKDTLFLPSRDATAPEPDA						
Qy	438 TS-RLRLYDKFEEEL-----GSRQEKAKARPPWEPPTKLUDEDESS						
Db	783 ESTITPKSVSDKDKRDKPKVKSDDTKRKSDGSAATKCONVULKPEKSGFOEKVQDGRKSP						
Qy	482 ESI---CSSEDST-----CSSSSSEFVDTIETRKKKHDPRLHDELMNDPQGM	5.3%					
Db	843 RSEBPLKQKEEATKIDSVKPSSSSQKDEKVGT-----PRKAHSKSAKUTRROSQPR--						
Qy	531 NDGPLKCSAKARRTIGIRSHIYFGEBAIKCPRPTNNAGRLHYRITSPPTWLTDRPT	5.0%					
Qy	896 -----TRSRKTRPKTS---SOKSQPVTRPRSLRKINY--LIAREKOKERERKK	9.1%					

GenCore version 5.1.7  
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Om protein - protein search, using sw model  
 Run on: February 3, 2006, 19:42:19 ; Search time 200 Seconds  
 (without alignments)

Scoring table: BLOSUM62 US-10-079-185-2  
 Gapop 10.0 , Gapext 0.5

Title: Perfect score: 7500

Sequence: 1 MMQGNTCHRMSTHPGRGCPGRGHHGARPSAPSFRQNLRLHQQPPVQYQEPSSA

Scanned: 1867569 seqs, 41782326 residues  
 Total number of hits satisfying chosen parameters: 1867569  
 Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries  
 Database : Published Applications AA Main:  
 1: /cgn2\_6/ptodata/1/pupaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/1/pupaa/US08\_PUBCOMB.pep:\*

3: /cgn2\_6/ptodata/1/pupaa/US09\_PUBCOMB.pep:\*

4: /cgn2\_6/ptodata/1/pupaa/US10\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/1/pupaa/US10\_PUBCOMB.pep:\*

6: /cgn2\_6/ptodata/1/pupaa/US10\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No. Score Query Length DB ID Description

Result No.	Score	Query	Length	DB	ID	Description
1	7500	100.0	1374	3	US-09-900-425A-2	Sequence 2, Appli
2	7500	100.0	1374	4	US-10-079-185-2	Sequence 2, Appli
3	7500	100.0	1374	4	US-10-074-974-2	Sequence 2, Appli
4	7500	100.0	1374	4	US-10-05-919-2	Sequence 2, Appli
5	7500	100.0	1374	6	US-11-001-995-2	Sequence 2, Appli
6	7486	99.8	1374	5	US-10-723-860-281	Sequence 281, Appli
7	7486	99.8	1374	5	US-10-756-149-4809	Sequence 4809, Appli
8	2963	39.9	1327	6	US-11-097-143-2409	Sequence 2409, Appli
9	2847	38.0	541	4	US-10-205-331-116	Sequence 116, Appli
10	2463	32.8	466	4	US-10-774-974-37	Sequence 37, Appli
11	1961	26.1	378	4	US-10-03-313-471	Sequence 471, Appli
12	1320	17.6	263	4	US-10-03-313-307	Sequence 307, Appli
13	890	11.9	412	3	US-09-900-425A-3	Sequence 3, Appli
14	890	11.9	412	4	US-10-079-185-3	Sequence 3, Appli
15	890	11.9	412	4	US-10-774-974-3	Sequence 3, Appli
16	890	11.9	412	4	US-10-805-919-3	Sequence 3, Appli
17	890	11.9	412	6	US-11-001-995-3	Sequence 3, Appli
18	340	4.5	1151	6	US-11-057-143-11586	Sequence 11586, Appli
19	311	4.1	560	5	US-10-457-563-51398	Sequence 51399, Appli
20	309.5	4.1	1557	4	US-10-477-963-13427	Sequence 137427, Appli
21	303.5	4.0	406	5	US-10-450-763-57609	Sequence 57609, Appli
22	298.5	4.0	237	4	US-10-437-963-13083	Sequence 130873, Appli
23	297.5	4.0	800	4	US-10-039-380-32198	Sequence 32198, Appli
24	292	3.9	466	4	US-10-437-963-167964	Sequence 167964, Appli
25	287.5	3.8	229	4	US-10-424-593-207316	Sequence 207316, Appli
26	285.5	3.8	258	4	US-10-437-963-159881	Sequence 159881, Appli
27	284.5	3.8	236	5	US-10-617-320-4394	Sequence 4394, Appli

#### ALIGNMENTS

RESULT 1  
 US-09-900-425A-2  
 Sequence 2, Application US/09900425A  
 ; Patent No. US20020164601A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wu, Hongjiang  
 ; INVENTOR: Crooke, Stanley T.  
 ; TITLE OF INVENTION: Human RNase III and Compositions and Uses Thereof  
 ; FILE REFERENCE: ISFH-0522  
 ; CURRENT APPLICATION NUMBER: US/09/900,425A  
 ; CURRENT FILING DATE: 2002-01-29  
 ; PRIORITY APPLICATION NUMBER: US 09/479,783  
 ; PRIORITY FILING DATE: 2000-01-07  
 ; PRIORITY FILING DATE: 1997-06-06  
 ; PRIORITY APPLICATION NUMBER: US 80/659,440  
 ; NUMBER OF SEQ ID NOS: 36  
 ; SOFTWARE: Patentin version 3.1  
 ; SEQ ID NO 2  
 ; LENGTH: 1374  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-900-425A-2  
 Query Match: 100.0%; Score: 7500; DB: 3; Length: 1374;  
 Best Local Similarity: 100.0%; Pred. No: 0; Mismatches: 0; Indels: 0; Gaps: 0;  
 Matches 1374; Conservative: 1  
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 Db 1 MMQGNTCHRMSTHPGRGCPGRGHHGARPSAPSFRQNLRLHQQPPVQYQEPSSA 60  
 Ov 61 TTFNSNSPAPNPLPRPDFVPPPPMPPSAQG3LPPCPIRPPFPNQHOMRHPVVPPCPFP 120  
 Db 61 TTFNSNSPAPNPLPRPDFVPPPPMPPSAQG3LPPCPIRPPFPNQHOMRHPVVPPCPFP 120  
 Ov 121 PPPMPCNNPPVPGAPPGQGTPFMPWPPSPHPPPPVPMQVQYPCYSHNFP 180  
 Db 121 PPPMPCNNPPVPGAPPGQGTPFMPWPPSPHPPPPVPMQVQYPCYSHNFP 180  
 Ov 181 SNSPQNPSSPLPSANNSSSPHFRLPYPLKADSRSRRPERLGHDDHRDHSGR 240  
 Db 181 SNSPQNPSSPLPSANNSSSPHFRLPYPLKADSRSRRPERLGHDDHRDHSGR 240  
 Ov 181 SNSPQNPSSPLPSANNSSSPHFRLPYPLKADSRSRRPERLGHDDHRDHSGR 240  
 Db 181 SNSPQNPSSPLPSANNSSSPHFRLPYPLKADSRSRRPERLGHDDHRDHSGR 240  
 Ov 241 GRRHSLDRRERGRSPDRRQDSRYSDDYDRGRTPSRHSRSRERERHRHRRRS 300  
 Db 241 GRRHSLDRRERGRSPDRRQDSRYSDDYDRGRTPSRHSRSRERERHRHRRRS 300  
 Ov 301 PSLSRSYKKEYRSRGSRSYGLSVPEPAGCTPBLPGSIIKNTDSWAPPLEIVNHRSPSREK 360

US-10-079-185-2

; Sequence 2, Application US/10079185

; Publication No. US20030044941A1

; GENERAL INFORMATION:

QY 361 KRARWEKEKDMSDNGSSGKDNYSIKEKEPEETMDKNEEEBLLKPVWIRCHSEN 420  
 Db 361 KRARWEKEKDMSDNGSSGKDNYSIKEKEPEETMDKNEEEBLLKPVWIRCHSEN 420  
 QY 421 YSSSDPMQVGSTVGTSLRDLYKFEELGSRQEAKARPPMEPKTLDELESS 480  
 Db 421 YSSSDPMQVGSTVGTSLRDLYKFEELGSRQEAKARPPMEPKTLDELESS 480  
 QY 481 SESECEDEDSTCSSSSDSEVFDVIAEIKRKKAHDRDLBWLWYNDPGQMDGPLCKSA 540  
 Db 481 SESECEDEDSTCSSSSDSEVFDVIAEIKRKKAHDRDLBWLWYNDPGQMDGPLCKSA 540  
 QY 541 KARRTGIRHSYYPEAKCPRPMTNAGRLHYRTVSPTNFLDRPTVIEYDHEYI 600  
 Db 541 KARRTGIRHSYYPEAKCPRPMTNAGRLHYRTVSPTNFLDRPTVIEYDHEYI 600  
 QY 601 FEGFSMMPAHAPLNPICKVIRPNIDTIHTEEMMPENFCVKGUBLSLFLFDILEYI 660  
 Db 601 FEGFSMMPAHAPLNPICKVIRPNIDTIHTEEMMPENFCVKGUBLSLFLFDILEYI 660  
 QY 661 DNKLKGFLFEDSPCCPRFHMIPRFVFLPDGKEVLSMHQILLYLVRCSGALVBEIA 720  
 Db 661 DNKLKGFLFEDSPCCPRFHMIPRFVFLPDGKEVLSMHQILLYLVRCSGALVBEIA 720  
 QY 721 NMLQWEEBLEWQYTAEBCKGMTVNPGRKPSSTRIDOLDRQNPDVITPPIVHFGIRPA 780  
 Db 721 NMLQWEEBLEWQYTAEBCKGMTVNPGRKPSSTRIDOLDRQNPDVITPPIVHFGIRPA 780  
 QY 781 QSYAGDPOYQOLKSVKLRILLANSPKVKDOKLAQREALKTQKONTMRETV 840  
 Db 781 QSYAGDPOYQOLKSVKLRILLANSPKVKDOKLAQREALKTQKONTMRETV 840  
 QY 841 EISSQGFWKGTGIRSDVQHAMLPLVTHIRHQCLMHDKLMIGYFQDRQCLLQAMTHP 900  
 Db 841 EISSQGFWKGTGIRSDVQHAMLPLVTHIRHQCLMHDKLMIGYFQDRQCLLQAMTHP 900  
 QY 901 SHHLNRFENKNDPDIARNSLNCGIRQPKYGRKTHMMARKKGINTLINSRLGQDPTPS 960  
 Db 901 SHHLNRFENKNDPDIARNSLNCGIRQPKYGRKTHMMARKKGINTLINSRLGQDPTPS 960  
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 Db 1021 FMYAHGPDCLCERDILRHAMANCPAFLIGAVLLEGSLBEAKQFLGRFLNPDREWLN 1080  
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 QY 1141 GHNORMERLGLDSIMOLVATEYFLIHPDHECHLTLSRSLVNRTOQAKVAELGMOEYA 1200  
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 QY 1201 ITNDKTKRPVGURKTLADLLESPIALYTDQLEYHTFMVCFPRPRKEFLNDWND 1260  
 Db 1201 ITNDKTKRPVGURKTLADLLESPIALYTDQLEYHTFMVCFPRPRKEFLNDWND 1260  
 QY 481 SESECEDEDSTCSSSSDSEVFDVIAEIKRKKAHDRDLBWLWYNDPGQMDGPLCKSA 540  
 Db 481 SESECEDEDSTCSSSSDSEVFDVIAEIKRKKAHDRDLBWLWYNDPGQMDGPLCKSA 540  
 QY 541 KARRTGIRHSYYPEAKCPRPMTNAGRLHYRTVSPTNFLDRPTVIEYDHEYI 600  
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 QY 601 FEGFSMMPAHAPLNPICKVIRPNIDTIHTEEMMPENFCVKGUBLSLFLFDILEYI 660  
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QY 661 DNLLKGPFEDSPCCPFHMPRFVFLPDLGKESVLSMHQIILYURCSKALVPEIA 720  
 Db 661 DNLLKGPFEDSPCCPFHMPRFVFLPDLGKESVLSMHQIILYURCSKALVPEIA 720  
 QY 721 NMLQWEELEWQKYAECKGMITNPGKPKSSRIDQDREQNDPVTIPITVHFGIRPA 780  
 Db 721 NMLQWEELEWQKYAECKGMITNPGKPKSSRIDQDREQNDPVTIPITVHFGIRPA 780  
 QY 781 QSYAGDPOYOKLWKSYKLRLANSPPKVOTDKOKLAOREALOKIROKTMRETV 840  
 Db 781 QSYAGDPOYOKLWKSYKLRLANSPPKVOTDKOKLAOREALOKIROKTMRETV 840  
 QY 841 ELSQGKWTGKRSVDYCHAMMLPVLTHIRHOCMLHDKLIGYFQDCLQLAMTHP 900  
 Db 841 ELSQGKWTGKRSVDYCHAMMLPVLTHIRHOCMLHDKLIGYFQDCLQLAMTHP 900  
 QY 901 SHHLNFGKMPDHARNSLSNCGRQPKYGRKTHMMRKKGGINTLIMSRLGODDPTS 960  
 Db 901 SHHLNFGKMPDHARNSLSNCGRQPKYGRKTHMMRKKGGINTLIMSRLGODDPTS 960  
 QY 961 RINHNERLEFLGDAVVEFLTSVHLYLPSLEGGLATYRATIVONHMLAKKELDP 1020  
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 QY 1021 FMYLYANGPDCRSBLAHAMANCFEAHLGAVLLEGSLBEAKOLFGRILFNDPDLREWLN 1080  
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 QY 1201 ITNDKTRPVGRTKTLADLUSPIALYTDQLEVHTFMVCFPFLKPERFLNODW 1260  
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 Db 1321 ENGAAMPALEKYNPQMAHQKPIGRKQREKEMRWEREHEOREPDETDKK 1374  
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 US-10-774-974-2  
 ; Sequence 2, Application US/10774974  
 ; Publication No. US20040126867A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wu, Hongjia Yang  
 ; APPLICANT: Crooke, Stanley T.  
 ; TITLE OF INVENTION: Human RNase III and Compositions and Uses Thereof  
 ; FILE REFERENCE: IS15029/1-SPH-0522  
 ; CURRENT APPLICATION NUMBER: US/10/774,974  
 ; CURRENT FILING DATE: 2004-02-09  
 ; PRIOR APPLICATION NUMBER: US/09/900,425B  
 ; PRIOR FILING DATE: 2001-07-06  
 ; NUMBER OF SEQ ID NOS: 37  
 ; SOFTWARE: Patentin version 3.1  
 ; SEQ ID NO 2  
 ; LENGTH: 1374  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-774-974-2  
 ; Query Match Score: 100.0%; DB: 4; Length: 1374;  
 ; Best Local Similarity: 100.0%; Pred. No. 0; Mismatches: 0; Indels: 0; Gaps: 0;  
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 QY 181 SFSNPNPSSLPSSANNSSPHRIPIPYLPKAFSRSRPERLKYDHHRHDSHGR 240  
 Db 181 SFSNPNPSSLPSSANNSSPHRIPIPYLPKAFSRSRPERLKYDHHRHDSHGR 240  
 QY 241 GHRHSRSLRERGRSPDRRDRDOSYRSYDSDYDGRGRTPSRHSRSYRSRSRERERERHRDRNRS 300  
 Db 241 GHRHSRSLRERGRSPDRRDRDOSYRSYDSDYDGRGRTPSRHSRSYRSRSRERERERHRDRNRS 300  
 QY 301 PSLSRSYKRSYGSYGLSVPEPAGCTPGLGEIKNTDSWAPPLEIVHRSRSRERERERHRDRNRS 360  
 Db 301 PSLSRSYKRSYGSYGLSVPEPAGCTPGLGEIKNTDSWAPPLEIVHRSRSRERERERHRDRNRS 360  
 QY 361 KJARWESEKDRNSDNQSSGKDKNTSKEKEFETMDKNEBEEELKPKWIRCHSEN 420  
 Db 361 KJARWESEKDRNSDNQSSGKDKNTSKEKEFETMDKNEBEEELKPKWIRCHSEN 420  
 QY 421 YSSSDPMQVGNTSTVVGTSRSLDLYDKFEEELGSRSOKAKARPMPWEPKTKLDELESS 480  
 Db 421 YSSSDPMQVGNTSTVVGTSRSLDLYDKFEEELGSRSOKAKARPMPWEPKTKLDELESS 480  
 QY 481 SISSECEDEDSTCSSLSSDSESEVDVIAKTKRKAHPDRLHSDLWYNPQGMNDGPKLCKSA 540  
 Db 481 SISSECEDEDSTCSSLSSDSESEVDVIAKTKRKAHPDRLHSDLWYNPQGMNDGPKLCKSA 540  
 QY 541 KARTGIRHSTYGPBEAKPCPRMTNAGRLFHRYRTSPPNFTDRPTVYDHEYI 600  
 Db 541 KARTGIRHSTYGPBEAKPCPRMTNAGRLFHRYRTSPPNFTDRPTVYDHEYI 600  
 QY 601 FEGFSMHPAHAPLNTIPICKVIRFNIDYTIHTEEMPEENFCVKGSLFSLFLFRDILEY 660  
 Db 601 FEGFSMHPAHAPLNTIPICKVIRFNIDYTIHTEEMPEENFCVKGSLFSLFLFRDILEY 660  
 QY 661 DNLLKGPFEDSPCCPFHMPRFVFLPDLGKESVLSMHQIILYURCSKALVPEIA 720  
 Db 661 DNLLKGPFEDSPCCPFHMPRFVFLPDLGKESVLSMHQIILYURCSKALVPEIA 720  
 QY 721 NMLQWEELEWQKYAECKGMITNPGKPKSSRIDQDREQNDPVTIPITVHFGIRPA 780  
 Db 721 NMLQWEELEWQKYAECKGMITNPGKPKSSRIDQDREQNDPVTIPITVHFGIRPA 780  
 QY 781 QSYAGDPOYOKLWKSYKLRLANSPPKVOTDKOKLAOREALOKIROKTMRETV 840  
 Db 781 QSYAGDPOYOKLWKSYKLRLANSPPKVOTDKOKLAOREALOKIROKTMRETV 840  
 QY 841 ELSQGKWTGKRSVDYCHAMMLPVLTHIRHOCMLHDKLIGYFQDCLQLAMTHP 900  
 Db 841 ELSQGKWTGKRSVDYCHAMMLPVLTHIRHOCMLHDKLIGYFQDCLQLAMTHP 900  
 QY 901 SHHLNFGKMPDHARNSLSNCGRQPKYGRKTHMMRKKGGINTLIMSRLGODDPTS 960  
 Db 901 SHHLNFGKMPDHARNSLSNCGRQPKYGRKTHMMRKKGGINTLIMSRLGODDPTS 960  
 QY 961 RINHNERLEFLGDAVVEFLTSVHLYLPSLEGGLATYRATIVONHMLAKKELDP 1020  
 Db 961 RINHNERLEFLGDAVVEFLTSVHLYLPSLEGGLATYRATIVONHMLAKKELDP 1020  
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 Db 1021 FMYLYANGPDCRSBLAHAMANCFEAHLGAVLLEGSLBEAKOLFGRILFNDPDLREWLN 1080

QY 1081 YPLHPIQLOENTDROLIETSPVLOKLTPEBAGIVFTVRLARAFTARTVGENHLT 1140  
 Db 1081 YPLHPIQLOEPNTDROLIETSPVLOKLTPEBAGIVFTVRLARAFTARTVGENHLT 1140  
 QY 1141 GHNORMEFLGSIMOLVATEYLFIRPDHMHGLTILRSVNNRTOAKVABELGNOYA 1200  
 Db 1141 GHNORMEFLGSIMOLVATEYLFIRPDHMHGLTILRSVNNRTOAKVABELGNOYA 1200  
 QY 1201 ITNDKTKRPGVSLRTKLADLLESFIALYLYTODKLEVYHTFMNCFFPRLKEFTLNDWND 1260  
 Db 1201 ITNDKTKRPGVSLRTKLADLLESFIALYLYTODKLEVYHTFMNCFFPRLKEFTLNDWND 1260  
 QY 1261 PKSQLQCCLTURTEGKEPDILYKLTQTVPSHARTYTAVYFKGERIGCKGKPSIQA 1320  
 Db 1261 PKSQLQCCLTURTEGKEPDILYKLTQTVPSHARTYTAVYFKGERIGCKGKPSIQA 1320  
 QY 1321 EMGAAMDALEKYNFPMQAHQKRFIGRKYRQELKEMWEREHOEREPDTEDIKK 1374  
 Db 1321 EMGAAMDALEKYNFPMQAHQKRFIGRKYRQELKEMWEREHOEREPDTEDIKK 1374

RESULT 4

US-10-805-919-2

; Sequence 2, Application US/10805919

; Publication No. US2004017582A1

; GENERAL INFORMATION:

APPLICANT: Wu, Hongjiang

APPLICANT: Croke, Stanley T.

TITLE OF INVENTION: Human RNase III and Compositions and Uses Thereof

FILE REFERENCE: ISPH-0522

CURRENT APPLICATION NUMBER: US/10/805,919

CURRENT FILING DATE: 2004-03-22

PRIOR APPLICATION NUMBER: US/09/900,425

PRIOR FILING DATE: 2001-07-06

PRIOR APPLICATION NUMBER: US 09/479,783

PRIOR FILING DATE: 2000-01-07

PRIOR APPLICATION NUMBER: US 08/870,608

PRIOR FILING DATE: 1997-06-06

PRIOR APPLICATION NUMBER: US 80/659,440

PRIOR FILING DATE: 1996-06-06

NUMBER OF SEQ ID NOS: 36

SOFTWARE: Patentin version 3.1

; SEQ ID NO 2

LENGTH: 1374

TYPE: PRT

; ORGANISM: Homo sapiens

US-10-805-919-2

Query Match 100.0%; Score 7500; DB 4; Length 1374;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGQNTCHRMSTHPGRGCPRGGGHARPSASFRPQLRLHQQPVQYQEPAPS 60  
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 QY 61 TTSNSNAPNFPFPRDPFVPPMPSAQGLPPCIRPPPNHQNRHPFPPCPHM 120  
 Db 61 TTSNSNAPNFPFPRDPFVPPMPSAQGLPPCIRPPPNHQNRHPFPPCPHM 120  
 QY 121 PRPMPCNPPPGAPGQGTPFMMPPSMHPPPVPMQVNTQPGSHRFPP 180  
 Db 121 PRPMPCNPPPGAPGQGTPFMMPPSMHPPPVPMQVNTQPGSHRFPP 180  
 QY 181 SNSPQNPSSPSLPSANSSSHPRHPPYPKASERSERLKEDYDHRDISHGR 240  
 Db 181 SNSPQNPSSPSLPSANSSSHPRHPPYPKASERSERLKEDYDHRDISHGR 240  
 QY 241 GHRHSRDRREGRSPDRRQPSRYSRDSYDROTPSRHRSRERERERHRDRNRS 300  
 Db 241 GHRHSRDRREGRSPRRQPSRYSRDSYDROTPSRHRSRERERERHRDRNRS 300

301 PSLERSVKKEYRSGRSYGLSVPEPAGCTPBLPGEIKNNTSWAPPLEIVNHRSPSREK 360

301 PSLERSVKKEYRSGRSYGLSVPEPAGCTPBLPGEIKNNTSWAPPLEIVNHRSPSREK 360

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601 FEGFSMFAHPLNTPLCKVIRFNIDYTHIEKMPENPCVKGLRLFLFRLFRDILEY 660

661 DNWLKGPLFEDSPCCPRFHMPPRFLPDKGKVELSMQIILYLRSCKALVBEIA 720

721 NMLQMBELEMOKYABECKGMIVTNFGTKRSVRDOLPDRQOFNPDVITFPTIVHFGIRPA 780

721 NMLQMBELEMOKYABECKGMIVTNFGTKRSVRDOLPDRQOFNPDVITFPTIVHFGIRPA 780

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781 QLSYAGDPPQOKLWYSYKURHLLANSPKQTKDQKLAQKIRONTMREVTV 840

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841 ELSQGFWKTCIRSVDYQHAMMLPULTHRYHOCMLHDLKIGTFQDCLLQAMTHP 900

901 SHHNLNGMNPDHARNSLNSNGCIRQPKYGDKVKHMEKRKGINTLINSRLQGDPTS 960

901 SHHNLNGMNPDHARNSLNSNGCIRQPKYGDKVKHMEKRKGINTLINSRLQGDPTS 960

Db 960

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1021 FMLAHGPDLCRESDRHARMANCEFLIGAVYLEGSLNEAKOLFGLLFUDPDRBWLN 1080

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1081 YPLHPIQLOENTDROLIETSPVLOKLTPEBAGIVFTVRLARAFTARTVGENHLT 1140

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1141 GHNORMEFLGSIMOLVATEYLFIRPDHMHGLTILRSVNNRTOAKVABELGNOYA 1200

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1201 ITNDKTKRPGVSLRTKLADLLESFIALYLYTODKLEVYHTFMNCFFPRLKEFTLNDWND 1260

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us-11-001-993-2 ; Application US/11001993  
; Sequence 2, Publication No. US20050159384A1  
; GENERAL INFORMATION:  
; APPLICANT: Crooke, Stanley T.  
; TITLE OF INVENTION: Human Rhase III And Compositions And Uses Thereof  
; FILE REFERENCE: ISIS003-104 (ISIS-5030US.D1)  
; CURRENT APPLICATION NUMBER: US/11/001,993  
; CURRENT FILING DATE: 2004-12-02  
; PRIORITY NUMBER: 10/079, 185  
; PRIORITY FILING DATE: 2002-02-20  
; PRIORITY APPLICATION NUMBER: 09/479, 783  
; PRIORITY FILING DATE: 2000-01-07  
; PRIORITY APPLICATION NUMBER: 08/870, 608  
; PRIORITY FILING DATE: 1997-06-06  
; PRIORITY APPLICATION NUMBER: 08/659, 440  
; PRIORITY FILING DATE: 1995-06-06  
; PRIORITY APPLICATION NUMBER: 09/900, 425  
; PRIORITY FILING DATE: 2001-07-06  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 1374  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-11-001-993-2

Query Match 100.0%; score 7500; DB 6; length 1374;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MNGQNTCHRMSTHPGRGCPRGQGHGARPSAQRSPNQLRHPQQPQVQYEPSPS 60  
Db 1 MNGQNTCHRMSTHPGRGCPRGQGHGARPSAQRSPNQLRHPQQPQVQYEPSPS 60  
Qy 61 TTFSNSTAPNFPRLPRDPDVFPFPMPMSAQGQLPPCIRRPPNQHMRPFPVPPCP 120  
Db 61 TTFSNSTAPNFPRLPRDPDVFPFPMPMSAQGQLPPCIRRPPNQHMRPFPVPPCP 120  
Qy 121 PPRMPCNCNPPPGAPGQGTPFMMPPSMHPPRPPVMPQVNTQYPPGSHHMPFP 180  
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Db 361 KGRARWEEKDRDSNOSSGKDNNTSKEKEBETMDKNEEEEEEELKPVWRCSEN 420  
Qy 421 YSSSDPMDQVGISTVGGTSRSLRDLYDKEEEIGSROEKAARAPPWEPKTCIILEDLESS 480  
Db 421 YSSSDPMDQVGISTVGGTSRSLRDLYDKEEEIGSROEKAARAPPWEPKTCIILEDLESS 480  
Qy 481 SRSCECSDEDSCSSSSDESEVDVIAEIKKAHPDHLDEWYNPQGMDGGLCKSCA 540  
Db 481 SRSCECSDEDSCSSSSDESEVDVIAEIKKAHPDHLDEWYNPQGMDGGLCKSCA 540  
Qy 541 KARRTGIRHSIYGEA1KPCPMTNAGRLHYRTVSPPNFLDRPTVYDHEYI 600  
Db 541 KARRTGIRHSIYGEA1KPCPMTNAGRLHYRTVSPPNFLDRPTVYDHEYI 600  
Qy 601 FGGFSMWAHAPLTNPICKVIRFNIDYTHEBEMMPENFCVKGLELFSLFRDILEY 660  
; Software: PatentIn version 3.2  
; SEQ ID NO 281  
; LENGTH: 1374  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-723-860-281

RESULT 6  
; Publication No. US20040253606A1  
; GENERAL INFORMATION:  
; APPLICANT: Aziz, Natasha  
; APPLICANT: Ginsburg, Wendy M.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions & File Reference: 05882\_0193.NFUS01  
; CURRENT APPLICATION NUMBER: US/10/723, 860  
; CURRENT FILING DATE: 2003-11-26  
; PRIORITY APPLICATION NUMBER: 60/429, 739  
; PRIORITY FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 8393  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 281  
; LENGTH: 1374  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-723-860-281

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Db 661 DMLKKGPFEDSPCCPCPFHFMRFVFLPDPGKEVTSMSHQILYLLRCSKALVPEBIA 720  
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Db 721 NMLOQWEELWQKAYAECKGMYTNPGRKPSYRVIDOLRQEPNPDVTPITVHFGIRPA 780  
Qy 781 QLSYAGDQYQKUWKSUTKURHLANSPKVKQTDQKLAQREBALQKIQKOTMRRETY 840  
Db 781 QLSYAGDQYQKUWKSUTKURHLANSPKVKQTDQKLAQREBALQKIQKOTMRRETY 840  
Qy 841 ELSQGFWKTGIRSDVOCAMMLPVLTIRYHQCLMFLDKLJGTYQDRCILQALWTHP 900  
Db 841 ELSQGFWKTGIRSDVOCAMMLPVLTIRYHQCLMFLDKLJGTYQDRCILQALWTHP 900  
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Db 901 SHHLNFGKNDPHARNSLNSCNGIRQPKYGRKVKVHMHKKGINTLIMSRLQDPPS 960  
Qy 961 RINHNEREFLGDAVFLTSILHLYKVPSPLEGGIATYRTATVQNHMLAKKEDP 1020  
Db 961 RINHNEREFLGDAVFLTSILHLYKVPSPLEGGIATYRTATVQNHMLAKKEDP 1020  
Qy 1021 FMYAHGDLCSDRHMANCFAELJGAVYLEGSLERAKOLFGRFLNDDDLREWWLN 1080  
Db 1021 FMYAHGDLCSDRHMANCFAELJGAVYLEGSLERAKOLFGRFLNDDDLREWWLN 1080  
Qy 1081 YRPLHPLQEPNTDROLJETSPVQKLTTEFEGIAVFLVTHYRLLAFTLRTVFGNHLT 1140  
Db 1081 YRPLHPLQEPNTDROLJETSPVQKLTTEFEGIAVFLVTHYRLLAFTLRTVFGNHLT 1140  
Qy 1141 GHNORMELFLGDSIMOLVATEYKPIHFDHHEGHTLIRSSUNRTOAKVAELGMOYA 1200  
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Db 1261 PSQLQOCCLTRTEGKEDPDLKYLQTCVGSHTARTVATYFKSERIGCGKGPSQOA 1320  
Qy 1321 EMGAAMDLEKKNPQMAKQKPIGKRYQELKEMWREEROBREPTEDKK 1374  
Db 1321 EMGAAMDLEKKNPQMAKQKPIGKRYQELKEMWREEROBREPTEDKK 1374



QY 361 KARWEEKEDRSRDSNQSGKDNYSIKEKEBETMPDKNEBEBELKPYWIRCHSEN 420  
 Db 361 KARWEEKEDRSRDSNQSGKDNYSIKEKEBETMPDKNEBEBELKPYWIRCHSEN 420  
 QY 421 YSSDPMQVGDSIVGTSRLDLYDKFEEBLSQEKAKARPPMEPKKUDLESS 480  
 Db 421 YSSDPMQVGDSIVGTSRLDLYDKFEEBLSQEKAKARPPMEPKKUDLESS 480  
 QY 481 SSECEDSSTCCESSDSEVVDIABIKRKKAHDPRLHDELYWYNDPGQMDGPLCKSA 540  
 Db 481 SSECEDSSTCCESSDSEVVDIABIKRKKAHDPRLHDELYWYNDPGQMDGPLCKSA 540  
 QY 541 KARRTGIRHSYIPEGEBAIKPCRPMTNAGRFHYRITVSPPNFLDRPTVYDHEYI 600  
 Db 541 KARRTGIRHSYIPEGEBAIKPCRPMTNAGRFHYRITVSPPNFLDRPTVYDHEYI 600  
 QY 601 FEGFSMRAHAPTNIPICKVIRFNIDTIEFEMBENPCVGRLEFLSLFLDITLEY 660  
 Db 601 FEGFSMRAHAPTNIPICKVIRFNIDTIEFEMBENPCVGRLEFLSLFLDITLEY 660  
 QY 661 DNKLKGPLFEDSPPCPFRHENVPRFLPDPGKEVLSMHOIILYLRCSKLVPEETIA 720  
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 Db 841 ELSQGFWKGTGSRDVQHANMPLVLTHTIRYQCLMHDKLGIGYTFODCQLQAMTHP 900  
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 Db 901 SHHLNFGMNPDARNLSNCNGRQPKYGRKHMNGKKGNTLINSLQGQDPTPS 960  
 QY 961 RINHNERLEFLGDAVVELTSYHLYLPPSLBEGGLATYRATIVONQHLMAMKBLDP 1020  
 Db 961 RINHNERLEFLGDAVVELTSYHLYLPPSLBEGGLATYRATIVONQHLMAMKBLDP 1020  
 QY 1021 FNLHYAHGPDLCRESLDRHMANCFAELIGAVLLEGSLBEAKOFLGRFLNDPDRREWLN 1080  
 Db 1021 FNLHYAHGPDLCRESLDRHMANCFAELIGAVLLEGSLBEAKOFLGRFLNDPDRREWLN 1080  
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 Db 1141 GHQRMEFLGSIMQVATEYFIRHFDHECHTLRSSLNNRTOQAKAELGQBEA 1200  
 QY 1141 GHQRMEFLGSIMQVATEYFIRHFDHECHTLRSSLNNRTOQAKAELGQBEA 1200  
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 QY 324 PRKARRVCKKHKSEACSSSSSSDDSDA-----PKLEQDCMEELSKVQH 373  
 Db 515 PQLHBLWYDQGMDGPKCSKARRGIRHSIPEGEBAIKPCRPMTNAGRFHY 574  
 Db 374 PQRVHADLWHDAGMDGPKCSKARRGIRHSIPEGEBAIKPCRPMTNAGRFHY 433  
 ; Sequence 2409, Application US/11097143  
 ; Publication No. US20050208558A1

RESULT 8  
 US-11-097-143-2409  
 ; Sequence 2409, Application US/11097143  
 ; Publication No. US20050208558A1

GENERAL INFORMATION:  
 APPLICANT: Venter, J. Craig  
 APPLICANT: et al.  
 TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID  
 TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE  
 TITLE OF INVENTION: DROSOPHILA GENES  
 FILE REFERENCE: CLO00728  
 CURRENT APPLICATION NUMBER: US/11/097,143  
 CURRENT FILING DATE: 2005-04-04  
 PRIORITY APPLICATION NUMBER: 60/157,832  
 PRIORITY FILING DATE: 1999-10-05  
 PRIORITY APPLICATION NUMBER: 60/160,191  
 PRIORITY FILING DATE: 1999-10-19  
 PRIORITY APPLICATION NUMBER: 60/161,932  
 PRIORITY FILING DATE: 1999-10-28  
 PRIORITY APPLICATION NUMBER: 60/164,769  
 PRIORITY FILING DATE: 1999-11-12  
 PRIORITY APPLICATION NUMBER: 60/173,383  
 PRIORITY FILING DATE: 1999-12-28  
 PRIORITY APPLICATION NUMBER: 60/175,693  
 PRIORITY FILING DATE: 2000-01-12  
 PRIORITY APPLICATION NUMBER: 60/184,831  
 PRIORITY FILING DATE: 2000-02-24  
 PRIORITY APPLICATION NUMBER: 60/191,637  
 PRIORITY FILING DATE: 2000-03-23  
 NUMBER OF SEQ ID NOS: 43008  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 2409  
 LENGTH: 1327  
 TYPE: PRT  
 ; ORGANISM: DROSOPHILA  
 US-11-097-143-2409  
 Query Match Similarity 39.5%; Score 2963; DB 6; Length 1327;  
 Best Local Similarity 45.8%; Pred. No. 7.8e-173; Gaps 32;  
 Matches 621; Conservative 213; Mismatches 327; Indels 200;  
 Db 90 QGQLPPCPIRPFPNQHMRHPPVPPCPFPMPMPMPCPN-NPPVPGAP-----P 137  
 Db 3 OPPUPPPVQPA-----P-----P-----P-----P-----P-----P-----P 137  
 QY 960 SHHLNFGMNPDARNLSNCNGRQPKYGRKHMNGKKGNTLINSLQGQDPTPS 960  
 Db 961 RINHNERLEFLGDAVVELTSYHLYLPPSLBEGGLATYRATIVONQHLMAMKBLDP 1020  
 Db 961 RINHNERLEFLGDAVVELTSYHLYLPPSLBEGGLATYRATIVONQHLMAMKBLDP 1020  
 QY 1020 FNLHYAHGPDLCRESLDRHMANCFAELIGAVLLEGSLBEAKOFLGRFLNDPDRREWLN 1080  
 Db 1020 FNLHYAHGPDLCRESLDRHMANCFAELIGAVLLEGSLBEAKOFLGRFLNDPDRREWLN 1080  
 QY 1080 PSFNSTQNPSPFLPSANNSSPHFLPPPL---PKAISERISPERLHYDHRD 235  
 Db 1080 PSFNSTQNPSPFLPSANNSSPHFLPPPL---PKAISERISPERLHYDHRD 235  
 QY 1081 YPLHPLQLOEPMTDROLIETSYLQKTEBFAIGVFTYHLLAFTRTGENHLT 1140  
 Db 1081 YPLHPLQLOEPMTDROLIETSYLQKTEBFAIGVFTYHLLAFTRTGENHLT 1140  
 QY 1140 SHHLNFGMNPDARNLSNCNGRQPKYGRKHMNGKKGNTLINSLQGQDPTPS 960  
 Db 1140 SHHLNFGMNPDARNLSNCNGRQPKYGRKHMNGKKGNTLINSLQGQDPTPS 960  
 QY 1140 GHQRMEFLGSIMQVATEYFIRHFDHECHTLRSSLNNRTOQAKAELGQBEA 1200  
 Db 1140 GHQRMEFLGSIMQVATEYFIRHFDHECHTLRSSLNNRTOQAKAELGQBEA 1200  
 QY 1200 ITNDKTRPVGRTKTLADLIESFIAALYDQKLEVYHMFVCFPLKKEFILNDWND 1260  
 Db 1200 ITNDKTRPVGRTKTLADLIESFIAALYDQKLEVYHMFVCFPLKKEFILNDWND 1260  
 QY 1260 PSQLQCCUTRTEGEKDPLYKLTQTVBSPHARTTYVWYKBRIGGKGSIQOA 1320  
 Db 1260 PSQLQCCUTRTEGEKDPLYKLTQTVBSPHARTTYVWYKBRIGGKGSIQOA 1320  
 QY 1320 ENGAAMDALEKYNPOMAHQKEFIGKRYQKEMRVEREHOBREDETEIKK 1374  
 Db 1320 ENGAAMDALEKYNPOMAHQKEFIGKRYQKEMRVEREHOBREDETEIKK 1374  
 QY 324 PRKARRVCKKHKSEACSSSSSSDDSDA-----PKLEQDCMEELSKVQH 373  
 Db 515 PQLHBLWYDQGMDGPKCSKARRGIRHSIPEGEBAIKPCRPMTNAGRFHY 574  
 Db 374 PQRVHADLWHDAGMDGPKCSKARRGIRHSIPEGEBAIKPCRPMTNAGRFHY 433



; ORGANISM: Homo sapiens  
; US-10-774-974-37

Query Match 32.8%; Score 2463; DB 4; Length 466;  
Best Local Similarity 100.0%; Pred. No. 9.9e-143;  
Matches 466; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 909 NPDHARNSLNSGIRQPKYGRDKVHMMRKGINTLNNMSRLGDDPTSPRINERL 968  
Db 1 NPDHARNSLNSGIRQPKYGRDKVHMMRKGINTLNNMSRLGDDPTSPRINERL 60

Qy 969 ERLGDAVEFLSIVHLTYLFRPLBEGSLATYTAIVONHQLAKLKEELDPMLYAHGP 1028  
Db 61 ERLGDAVEFLTSVHLVLYLFPSPLEGGLATYTAIVONHQLAKLKEELDPMLYAHGP 120

Qy 1029 DCRESDRHAMANCEFALIGVYLEGSLEEKQKQLERLFLDPUREWVNYTPIRQL 1088  
Db 121 DCRESDRHAMANCEFALIGVYLEGSLEEKQKQLERLFLDPUREWVNYTPIRQL 180

Qy 1089 QEPNTDQLIETSPVLOKTEBAAIGVIFTNLLARAFTRTGVGENHLTGHNORMEF 1148

Db 181 QEPNTDQLIETSPVLOKTEBAAIGVIFTNLLARAFTRTGVGENHLTGHNORMEF 240

Qy 1149 LGDSIMOLVATYLFHIFPDRHFGHLTLRSLLSVLNNRTOQVAAEGLGMOEYAITNDTKR 1208  
Db 241 LGDSIMOLVATYLFHIFPDRHFGHLTLRSLLSVLNNRTOQVAAEGLGMOEYAITNDTKR 300

Qy 1209 PGVLRLTKTLADLIESFIALYTDKOLEYHTMNCFPRKLFIFINQDWDPKSOLQOC 1268  
Db 301 PGVLRLTKTLADLIESFIALYTDKOLEYHTMNCFPRKLFIFINQDWDPKSOLQOC 360

Qy 1269 CILTRTEGKEPDILPKLQLTGPGSHARTYTVAVYFKGERIGCGKGPSIQQAEMGANDMA 1328  
Db 361 CILTRTEGKEPDILPKLQLTGPGSHARTYTVAVYFKGERIGCGKGPSIQQAEMGANDMA 420

Qy 1329 LKYNFQOMAOKRFLCKYRKEBLKEMRWERHQEREPDTEDEIKK 1374  
Db 421 LKYNFQOMAOKRFLCKYRKEBLKEMRWERHQEREPDTEDEIKK 466

RESULT 11  
US-10-103-313-471

Sequence 471, Application US/10103313  
; Publication No. US20030082758A1

; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PUS07C1  
; CURRENT APPLICATION NUMBER: US/10/103,313

; CURRENT FILING DATE: 2002-03-12  
; NUMBER OF SEQ ID NOS: 653

; Prior Application removed - See File Wrapper or Palm  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO: 307  
; LENGTH: 263

; TYPE: PRT  
; ORGANISM: Homo sapiens

US-10-103-313-307

Query Match 17.6%; Score 1320; DB 4; Length 263;  
Best Local Similarity 97.7%; Pred. No. 6.7e-73; Matches 251; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1118 ETRHVLARAFTRTGVFHNLTGHNORMERLFLGDSIMOLVATEYIFHIFPDRHFGHLTL 1177  
Db 7 FYSCLLRAFTLRTVGFHNLTGHNORMERLFLGDSIMOLVATEYIFHIFPDRHFGHLTL 66

Qy 1178 RSSLNNRTOQVAAEGLGMOEYAITNDTKRPGVLRLTKTLADLIESFIALYTDKOLEY 1237  
Db 67 RSSLNNRTOQVAAEGLGMOEYAITNDTKRPGVLRLTKTLADLIESFIALYTDKOLEY 126

Qy 1238 HTFMNYCFFPRKLFIFINQDWDPKSOLQOCCLTARTEGKEPDILPKLQLTGPGSHART 1297  
Db 127 HTFMNYCFFPRKLFIFINQDWDPKSOLQOCCLTARTEGKEPDILPKLQLTGPGSHART 186

Qy 1298 YTVAVYFKGERIGCGKGPSIQQAEMGANDMALEKYNFQOMAOKRFLCKYRKEBLKEMR 1357  
Db 187 YTVAVYFKGERIGCGKGPSIQQAEMGANDMALEKYNFQOMAOKRFLCKYRKEBLKEMR 246

Qy 1358 EREHQSRPDEDEIKK 1374  
Db 247 EREHQSRPDEDEIKK 263

Query Match 26.1%; Score 1961; DB 4; Length 378;  
Best Local Similarity 98.9%; Pred. No. 4.9e-112; Matches 374; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

RESULT 13  
US-09-900-425A-3  
; Sequence 3, Application US/09900425A  
; Patent No. US20020164601A

; GENERAL INFORMATION:  
; APPLICANT: Wu, Hongjiang

; TITLE OF INVENTION: Human RNase III and Compositions and Uses Thereof

; FILE REFERENCE: ISPH-0522  
; CURRENT APPLICATION NUMBER: US/09/900,425A

Db 121 ITRHVLARAFTRTGVFHNLTGHNORMERLFLGDSIMOLVATEYIFHIFPDRHFGHLTL 180  
Qy 1117 LRSLSVNRTOQVAAEGLGMOEYAITNDTKRPGVLRLTKTLADLIESFIALYTDKOLEY 1236  
Db 181 LRSLSVNRTOQVAAEGLGMOEYAITNDTKRPGVLRLTKTLADLIESFIALYTDKOLEY 240

Qy 1237 VTFPMNYCFFPRKLFIFINQDWDPKSOLQOCCLTARTEGKEPDILPKLQLTGPGSHAR 1296  
Db 241 VTFPMNYCFFPRKLFIFINQDWDPKSOLQOCCLTARTEGKEPDILPKLQLTGPGSHAR 300

Qy 1297 YTVAVYFKGERIGCGKGPSIQQAEMGANDMALEKYNFQOMAOKRFLCKYRKEBLKEMR 1356  
Db 301 YTVAVYFKGERIGCGKGPSIQQAEMGANDMALEKYNFQOMAOKRFLCKYRKEBLKEMR 360

Qy 1357 WEREHQSRPDEDEIKK 1374  
Db 361 WEREHQSRPDEDEIKK 378

Qy 1117 LRSLSVNRTOQVAAEGLGMOEYAITNDTKRPGVLRLTKTLADLIESFIALYTDKOLEY 1236  
Db 181 LRSLSVNRTOQVAAEGLGMOEYAITNDTKRPGVLRLTKTLADLIESFIALYTDKOLEY 240

Qy 1117 LRSLSVNRTOQVAAEGLGMOEYAITNDTKRPGVLRLTKTLADLIESFIALYTDKOLEY 1236  
Db 181 LRSLSVNRTOQVAAEGLGMOEYAIT

CURRENT FILING DATE: 2002-01-29  
 PRIORITY APPLICATION NUMBER: US 09/479, 783  
 PRIORITY FILING DATE: 2000-01-07  
 PRIORITY APPLICATION NUMBER: US 08/870, 608  
 PRIORITY FILING DATE: 1997-06-06  
 NUMBER OF SEQ ID NOS: 36  
 SOFTWARE: Patentin version 3.1  
 SEQ ID NO 3  
 LENGTH: 412  
 TYPE: PRT  
 ORGANISM: *Caenorhabditis elegans*  
 US-09-900-425A-3

Query Match 11.9%; Score 890; DB 3; Length 412;  
 Best Local Similarity 43.1%; Pred. No. 3e-46;  
 Matches 181; Conservative 85; Mismatches 136; Indels 18; Gaps 7;

Beet Local Similarity 43.1%; Pred. No. 3e-46; Mismatches 136; Indels 18; Gaps 7;  
 Matches 181; Conservative 85; Mismatches 136; Indels 18; Gaps 7;

Qy 944 TLINIMSRGLGDDPPSRINNERRFLGAVVERLTSVLYLFLPSLESGLATYTAI 1003  
 Db 2 SLFNMKGTSGGEP---TLHNERLEYIGDAVVELVSHHLYFMLTHFEGGLATYTAI 1003  
 Qy 1004 VONQHMLAMKLEDPFMLYAHGDLICRSDLRHAMANCEFLALGAVYIYEGSLEAKQL 1063  
 Db 58 VONRNLATLAKNCRIDEMLQYSHGADLINVAFKHLANAEFAWAAIVDGGLAPCDVI 117  
 Qy 1064 FGRLLF-NDPDREWLNYPHLPLQLOEPNDROLIETSPVNLQKLTFSRIGVIFTHR 1122  
 Db 118 FSKAMYGHQPVLEKEWDHINHELKEPDQCDRDLSPITPTFHALLERLGIQPNIR 177  
 Qy 1123 LLARAFTRTGVPHNLTGHNORMFLGISMOLVATEVIFHFDPHEGHTLASSLV 1182  
 Db 178 LLAKAFTTRNIPNNDLTGHNORLEWLGDSVQLIVSDFLYRFRFPYHEGHMSLRTSLV 237  
 Qy 1183 NNRTOQAVAEELGMQEVAITNDKTKRVE--GLRTKTLADLESITALYTDKDLIEVHT 1182  
 Db 1240 FNNVCFPPLKEFILQNDPKSOLQOCCLTR-TEGKEDDIPLYKTQVGPShARTY 1298  
 Qy 293 FIRIVFCPRLKHFIESEKWNDAKSHLQCLAMRDSSPDSSBPDMPYRVLGIEGPNTNR 352  
 Db 1299 TVAVYFKGERIGCGKGPSIQQAEMGA--IMDALEKNPQFOM-AHQKRFGRKYQELKE 1354  
 Db 353 KIAVYVKGKRLASAESAESNVHKAELRVAELALANLESMSFSKMKAKNSNMRRLBQSTD 412

RESULT 14  
 US-10-079-185-3  
 Sequence 3, Application US/10079185  
 Publication No. US20030044941A1

GENERAL INFORMATION:  
 APPLICANT: Wu, Hongjiang  
 APPLICANT: Cooke, Stanley T.  
 TITLE OF INVENTION: Human RNase III And Compositions And Uses Thereof  
 FILE REFERENCE: IS15029/ISPA-0522  
 CURRENT APPLICATION NUMBER: US10/774,974  
 CURRENT FILING DATE: 2004-02-09  
 PRIORITY APPLICATION NUMBER: US/09/900,425B  
 PRIORITY FILING DATE: 2001-07-06  
 NUMBER OF SEQ ID NOS: 37  
 SOFTWARE: Patentin version 3.1  
 SEQ ID NO 3  
 LENGTH: 412  
 TYPE: PRT  
 ORGANISM: *Caenorhabditis elegans*  
 US-10-774-974-3

Query Match 11.9%; Score 890; DB 4; Length 412;  
 Best Local Similarity 43.1%; Pred. No. 3e-46;  
 Matches 181; Conservative 85; Mismatches 136; Indels 18; Gaps 7;

TITLE OF INVENTION: Human RNase III And Compositions And Uses Thereof  
 FILE REFERENCE: IS15029/ISPA-0522  
 CURRENT APPLICATION NUMBER: US/10/774,974  
 CURRENT FILING DATE: 2004-02-09  
 PRIORITY APPLICATION NUMBER: US/09/900,425B  
 PRIORITY FILING DATE: 2001-07-06  
 NUMBER OF SEQ ID NOS: 36  
 SOFTWARE: Patentin version 3.1  
 SEQ ID NO 3  
 LENGTH: 412  
 TYPE: PRT  
 ORGANISM: *Caenorhabditis elegans*  
 US-10-079-185-3

Query Match 11.9%; Score 890; DB 4; Length 412;  
 Best Local Similarity 43.1%; Pred. No. 3e-46;  
 Matches 181; Conservative 85; Mismatches 136; Indels 18; Gaps 7;

Beet Local Similarity 43.1%; Pred. No. 3e-46; Mismatches 136; Indels 18; Gaps 7;  
 Matches 181; Conservative 85; Mismatches 136; Indels 18; Gaps 7;

Qy 944 TLINIMSRGLGDDPPSRINNERRFLGAVVERLTSVLYLFLPSLESGLATYTAI 1003  
 Db 2 SLFNMKGTSGGEP---TLHNERLEYIGDAVVELVSHHLYFMLTHFEGGLATYTAI 1003  
 Qy 1004 VONQHMLAMKLEDPFMLYAHGDLICRSDLRHAMANCEFLALGAVYIYEGSLEAKQL 1063  
 Db 58 VONRNLATLAKNCRIDEMLQYSHGADLINVAFKHLANAEFAWAAIVDGGLAPCDVI 117  
 Qy 1064 FGRLLF-NDPDREWLNYPHLPLQLOEPNDROLIETSPVNLQKLTFSRIGVIFTHR 1122  
 Db 118 FSKAMYGHQPVLEKEWDHINHELKEPDQCDRDLSPITPTFHALLERLGIQPNIR 177  
 Qy 1123 LLARAFTRTGVPHNLTGHNORMFLGISMOLVATEVIFHFDPHEGHTLASSLV 1182  
 Db 178 LLAKAFTTRNIPNNDLTGHNORLEWLGDSVQLIVSDFLYRFRFPYHEGHMSLRTSLV 237  
 Qy 1183 NNRTOQAVAEELGMQEVAITNDKTKRVE--GLRTKTLADLESITALYTDKDLIEVHT 1239  
 Db 238 SNOTQAVWCODLGFPEFV---KAPYKPEBLKOKDADLVEATGALYVDRGHEHCA 292  
 Qy 1240 FNNVCFPPLKEFILQNDPKSOLQOCCLTR-TEGKEDDIPLYKTQVGPShARTY 1298  
 Db 293 FIRIVFCPRLKHFIESEKWNDAKSHLQCLAMRDSSPDSSBPDMPYRVLGIEGPNTNR 352  
 Qy 1299 TVAVYFKGERIGCGKGPSIQQAEMGA--IMDALEKNPQFOM-AHQKRFGRKYQELKE 1354  
 Db 353 KIAVYVKGKRLASAESAESNVHKAELRVAELALANLESMSFSKMKAKNSNMRRLBQSTD 412

RESULT 15  
 US-10-774-974-3  
 Sequence 3, Application US/10774974  
 Publication No. US20040126867A1

GENERAL INFORMATION:  
 APPLICANT: Wu, Hongjiang  
 APPLICANT: Cooke, Stanley T.  
 TITLE OF INVENTION: Human RNase III And Compositions And Uses Thereof  
 FILE REFERENCE: IS15029/ISPA-0522  
 CURRENT APPLICATION NUMBER: US/10/774,974  
 CURRENT FILING DATE: 2004-02-09  
 PRIORITY APPLICATION NUMBER: US/09/900,425B  
 PRIORITY FILING DATE: 2001-07-06  
 NUMBER OF SEQ ID NOS: 37  
 SOFTWARE: Patentin version 3.1  
 SEQ ID NO 3  
 LENGTH: 412  
 TYPE: PRT  
 ORGANISM: *Caenorhabditis elegans*  
 US-10-774-974-3

Query Match 11.9%; Score 890; DB 4; Length 412;  
 Best Local Similarity 43.1%; Pred. No. 3e-46;  
 Matches 181; Conservative 85; Mismatches 136; Indels 18; Gaps 7;

Beet Local Similarity 43.1%; Pred. No. 3e-46; Mismatches 136; Indels 18; Gaps 7;  
 Matches 181; Conservative 85; Mismatches 136; Indels 18; Gaps 7;

Qy 944 TLINIMSRGLGDDPPSRINNERRFLGAVVERLTSVLYLFLPSLESGLATYTAI 1003  
 Db 2 SLFNMKGTSGGEP---TLHNERLEYIGDAVVELVSHHLYFMLTHFEGGLATYTAI 1003  
 Qy 1004 VONQHMLAMKLEDPFMLYAHGDLICRSDLRHAMANCEFLALGAVYIYEGSLEAKQL 1063  
 Db 58 VONRNLATLAKNCRIDEMLQYSHGADLINVAFKHLANAEFAWAAIVDGGLAPCDVI 117  
 Qy 1064 FGRLLF-NDPDREWLNYPHLPLQLOEPNDROLIETSPVNLQKLTFSRIGVIFTHR 1122  
 Db 118 FSKAMYGHQPVLEKEWDHINHELKEPDQCDRDLSPITPTFHALLERLGIQPNIR 177  
 Qy 1123 LLARAFTRTGVPHNLTGHNORMFLGISMOLVATEVIFHFDPHEGHTLASSLV 1182

Db 178 LLAKAFTRRNTPNNNDTKGHMQRLEMLGDSVQLQIVSDFLYRFPYTHEGMSLRTSLV 237  
Qy 1183 NNRTOAQVAEELGMOEVAITNDKTKEPV--GLRTKTYLADLIESPAALYTDKDLIYVHT 1239  
Db 238 SNOTQAWCDDLGFTEFVI----KAPYKTEFLKLKDADLWEAFIGALYVDRGIEHCRA 292  
Qy 1240 FNNVCFFPRLKEFILMNDWNPKSQIQCCLTR-TEGKEDDIPLYKTLQWGSPARTY 1298  
Db 293 FTRIVFCPRLKHFIESBKWNDAKSHLQOWCLMRDPSSSEPIMPEYRVLGIEGPTNRF 352  
Qy 1299 TVAVYFKGERIGCGKGPSIQQLEMGA--AMDALEKYNPQM-AHQKRFIGRKYROELKE 1354  
Db 353 KIAVYYKGKRLASAESAESNVHKELVAAELALANLESMSFSKAKONSNMRLEQDTSD 412

Search completed: February 3, 2006, 19:46:38  
Job time : 206 secs

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## **Protein Sequence Searches - February 2005**

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

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GenCore version 5.1.7  
 Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 3, 2006, 19:43:20 ; Search time 16 Seconds

Perfect Score: 7500

Sequence: US-10-079-185-2

1 MMQNCNTCHRMSSFHGRGCPK. .... MRRWREHQHQPDPEDIEKK 1374 (without alignments)

1006.288 Million cell updates/sec

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 88029 seqs, 11718060 residues

Total number of hits satisfying chosen parameters: 88029

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Published Applications AA New:\*

1: /cgn2\_6/ptodata/2/pupaa/US06\_NEW\_PUB.pep:\*

2: /cgn2\_6/ptodata/2/pupaa/US06\_NEW\_PUB.pep:\*

3: /cgn2\_6/ptodata/2/pupaa/US07\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/2/pupaa/PCT\_NEW\_PUB.pep:\*

5: /cgn2\_6/ptodata/2/pupaa/US09\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/2/pupaa/US10\_NEW\_PUB.pep:\*

7: /cgn2\_6/ptodata/2/pupaa/US11\_NEW\_PUB.pep:\*

8: /cgn2\_6/ptodata/2/pupaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1  
 US-10-523-477-14

; Sequence 14, Application US/10523477  
 ; Publication No. US20050266406A1

; GENERAL INFORMATION:

; APPLICANT: EXELIXIS, INC.

; TITLE OF INVENTION: MAX AS MODIFIERS OF THE AXIN PATHWAY AND METHODS OF USE

; FILE REFERENCE: EX03-051C-US

; CURRENT APPLICATION NUMBER: US/10-523,477

; CURRENT FILING DATE: 2005-02-04

; PRIOR APPLICATION NUMBER: US 60/401,534

; PRIOR FILING DATE: 2002-08-07

; PRIOR APPLICATION NUMBER: US 60/411,153

; PRIOR FILING DATE: 2002-09-16

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 14

; LENGTH: 948

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-523-477-14

Query Match 3.7%; Score 276; DB 6; Length 948;  
 Best Local Similarity 23.0%; Pred. No. 4e-10; Mismatches 208; Indels 230; Gaps 31;  
 Matches 149; Conservative 61; Mismatches 208; Indels 230; Gaps 31;

QY 27 ARPSA- PSFRPQNLRLHPPQQPVQYQEPSSA----- PSTDTSNSPAPNFLPR 75

Db 320 ARPGGGCGCGKKGKLVLSPPQIQRGERSCYRSNRGRHHSRSORTQDPS-LPAT 377

QY 76 DDFVFPFPMPMPSAQGQLPCLPCCRPPFHQMRHFPVPPCPEPMPPNPCKPNPPVGA 135

Db 378 PVFVFPVPP-----PLVPPP---HTLPLP-----PQVPPQFSPQPP--PQQ 415

QY 136 PEGQSTETPMMRPPSPMHPPPPPMPOQVN-----YQVPP----- 170

Db 416 PPGAG--YSPVPPGPG-PAPANLSTPWAQVTAHSNTIPTQAPPLSEREPYREORR 471

QY 171 -----GSHHNNPPPSFTS 184

Db 472 KKEBEKKKSKLDFNTNDFAKELMVKKIQKERRRSFSRSKSPGSSYSSRSVYSKRS 531

QY 185 QKNNPSSPAPANSSSHFRHLPPVPAKAPBRSRSPRLKDDHHRDHSRGERK 244

Db 532 GSTRSRSTSRFSRSHRSYSRSPYR----RGRGKSRV--RSRSRSHG--YH 578

QY 245 RSDURREGRSPRQRDRSRSYSDY-RGRTPSRHSRSYRSRER----- 289

ALIGNMENTS

RESULT 3

US-11-150-845-40

; Sequence 40, Application US/11150845

; Publication No. US200601033961

; GENERAL INFORMATION:

QY 634 AYGRSVDPRPFKEKERYE-----WERKREWYKYGAGQPRFSA----- 679

Db 337 IIXNNTISWAP---PEIYHNRSPREKKRRAWEEDKDRMSDDNOSSG-----KD 381

QY 680 ---NRENFSPEPFLPLNIRN-SPFTRGRREYGGOSHRNRSNTPKLSARDGHNQ 734

QY 382 KNTSIKEKEPEBTMPD-----KREBEBELKWKWIRCHSENWYSSDPM- 427

Db 735 KNTTKKEKESEBNAPGDGKGNHKKRKRRKGKESBGGFLNPELETSRK---SRPTGV 790

QY 428 -DQVGISTVVGTSR---LRDLYDKFEE--LGRQEKAKAARDPWEPPRKUDDELE 478

Db 791 BENTKTSLFLVPLRSRDAIPVRD-EPMDAESTPKSVSEKDRR---DKEPKAKDITR 845

QY 479 SSSESCCESBESDSTC5SSSDS-----VFDVIAIBKREKAHPDRL 518

Db 846 KNDGSAVSKKENIVKPKAGPQKVVDGVDLNLQNLQKDKRRRLRL 893

RESULT 2

US-10-793-626-1658

; Sequence 1658, Application US/10793626

; Publication No. US20050255478A1

; GENERAL INFORMATION:

APPLICANT: KIMMELLY, WILLIAM JOHN

TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

FILE REFERENCE: PU34805

CURRENT APPLICATION NUMBER: US/10/793, 626

CURRENT FILING DATE: 2004-03-04

PRIOR APPLICATION NUMBER: 60/164, 258

PRIOR FILING DATE: 1999-11-09

NUMBER OF SEQ ID NOS: 4472

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 1658

LENGTH: 245

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: SCAR2

OTHER INFORMATION: Description of Artificial Sequence: synthetic

OTHER INFORMATION: amino acid sequence

US-10-793-626-1658

Query Match 3.5%; Score 260.5; DB 6; Length 245;

Best Local Similarity 30.4%; Pred. No. 7.2e-10;

Matches 70; Conservative 57; Mismatches 88; Indels 15; Gaps 8;

Matched 70;

Query 1105 QKLTTEFAAIGVIFTYHLLAAPTLLTV-GFNHLITLGHQMRMELTGDSIMQVATEYL 1162

Db 15 QKFTDKOMSLGFLRKNQDLYQQAFSHSSINDFNMRLEHQRLETLGAVLTVSRYL 74

QY 1163 FHHPPDHHEGHATLRLRSVNNRTOQKVAEELGMQEAITNDKTRKPVGLRK-TIADL 1220

Db 75 FDRPHPHLPEGNLTMRATIVCPSLVLFANKIKLNEELLG-KGEETGGRTRPSLSDA 133

QY 1221 LPSFLALYTDPLLEVYHTEMVCPFPLRK-EFLINQDWDNPKSQDQOCITLRVGEKE 1278

Db 134 PFAFVGALYDQDLSWTFAKVYIFVYEDDLVGVVDF--KTOPOE--YVHSQN- 186

QY 1279 PDIPLYKILQTFGSHARTYTAVYFKGERICGGKGKGSIQQEMGAMDA 1328

Db 187 GIV-TYOLIKEGPAHRLTSEVILENKAVWEGKAKTKKSESEQAEQA 235

RESULT 4

US-11-149-945-4

; Sequence 4, Application US/11119945

; Publication No. US2006014266A1

; GENERAL INFORMATION:

APPLICANT: Cytokinetics, Inc.

APPLICANT: Tomasevic, Nenad

APPLICANT: Sakowicz, Roman

TITLE OF INVENTION: PURIFICATION OF ARP2/3 COMPLEX

TITLE OF INVENTION: PURIFIED ARP2/3 COMPLEX

FILE REFERENCE: 020552-007810US

CURRENT APPLICATION NUMBER: US/11/49, 945

CURRENT FILING DATE: 2005-06-10

PRIOR APPLICATION NUMBER: US 60/578, 969

PRIOR FILING DATE: 2004-06-10

NUMBER OF SEQ ID NOS: 11

SOFTWARE: PatentIn version 3.3

SEQ ID NO: 4

LENGTH: 498

TYPE: PRT

ORGANISM: Homo sapiens

US-11-149-945-4



RESULT 7  
US-11-150-845-3  
; Sequence 38, Application US/11150845  
; Publication No. US20060033399A1  
; GENERAL INFORMATION:  
; APPLICANT: Cytokinetics, Inc.  
; APPLICANT: Tomasevic, Nenad  
; APPLICANT: Jia, Zhiheng  
; APPLICANT: Sakowicz, Roman  
; APPLICANT: Pierce, Daniel  
; TITLE OF INVENTION: HIGH THROUPUT ACTIN POLYMERIZATION ASSAY  
; FILE REFERENCE: 020552-007720US  
; CURRENT FILING DATE: 2005-06-10  
; PRIORITY APPLICATION NUMBER: US 60/673,444  
; PRIORITY FILING DATE: 2005-04-20  
; PRIORITY FILING DATE: 2004-06-10  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 3  
; LENGTH: 559  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-11-149-945-3  
; Query Match 2.8%; Score 211.5; DB 7; Length 559;  
; Best Local Similarity 25.7%; Pred. No. 2.7e-06;  
; Matches 86; Conservative 30; Mismatches 111; Indels 107; Gaps 16;  
; Matches 86; Conservative 30; Mismatches 111; Indels 107; Gaps 16;  
; QY 35 RPPONRLRLLHQPPQPVQYQEP-----SAPSTTFNSNP-----APNFL 72  
; Db 266 RASERVLVYRPHEP-----PPPPMHAGDAKPIPTCISATTGLIENRQFQSPATGRTPVRV 320  
; QY 73 PPRDFVFRPPRPPRPSA-----QGPLPCKPIRPPFNPQMRIFPPVPCFP-----118  
; Db 321 SPTP-----PPPPPLPSALSTSRLRASMTSTPPPPVPPPPVPPPPVPPAPLQI 377  
; QY 119 -----PMPPPMPC-----NNPPVPGAGPQGQTTPFMMPP-----SMPPPPPPVMPQV 164  
; Db 378 ACPVULHPAPPPLAPVQPSPPVAAVAPVCTEP-----VHLRQEVGQGLPPPPVPPAPLQI 433  
; QY 165 NYQVPPGYSHHNFPFPSTNSFQNNPSFLPSANNNSSPHFRPPY-----LPKAPSERR 220  
; Db 434 -----PPGIRPS-----PVTALAHPPSGLHPTSTAGPHVPLWPPSPSPQVIP-ASEPGR 486  
; OTHER INFORMATION: SCAR1/WAVE1  
; US-11-150-845-38  
; Query Match 2.8%; Score 211.5; DB 7; Length 559;  
; Best Local Similarity 25.7%; Pred. No. 2.7e-06;  
; Matches 86; Conservative 30; Mismatches 111; Indels 107; Gaps 16;  
; QY 35 RPPONRLRLLHQPPQPVQYEP-----SAPSTTFNSNP-----APNFL 72  
; Db 266 RABERVLVYRPHEP-----PPPMHAGDAKPIPTCISATTGLIENRQFQSPATGRTPVRV 320  
; QY 73 PPRDFVFRPPRPPRPSA-----QGPLPCKPIRPPFNPQMRIFPPVPCFP-----118  
; Db 321 SPTP-----PPPPPLPSALSTSRLRASMTSTPPPPVPPPPVPPPPVPPAPLQI 377  
; QY 119 -----PMPPPMPC-----NNPPVPGAGPQGQTTPFMMPP-----SMPPPPPPVMPQV 164  
; Db 378 ACPVULHPAPPPLAPVQPSPPVAAVAPVCTEP-----VHLRQEVGQGLPPPPVPPAPLQI 433  
; QY 165 NYQVPPGYSHHNFPFPSTNSFQNNPSFLPSANNNSSPHFRPPY-----LPKAPSERR 220  
; Db 434 -----PPGIRPS-----PVTALAHPPSGLHPTSTAGPHVPLWPPSPSPQVIP-ASEPGR 486  
; OTHER INFORMATION: SCAR1/WAVE1  
; US-11-149-945-3  
; Query Match 2.8%; Score 211.5; DB 7; Length 559;  
; Best Local Similarity 25.7%; Pred. No. 2.7e-06;  
; Matches 86; Conservative 30; Mismatches 111; Indels 107; Gaps 16;  
; Matches 86; Conservative 30; Mismatches 111; Indels 107; Gaps 16;  
; QY 221 SPERLKHYDDHRHRSRGRGERRSRDRRSRQDSRYSYDGRGTPRSRS 280  
; Db 487 HPSLTPVSD-----ANSVLAIRKG-----IQLRK 513  
; QY 281 YERSRERERHRHRHNRSPSLRSRSYKEYKRS 314  
; Db 514 VEEQEQE-AKHERIENDVATLSRRIAVEYSDS 546  
; Db 514 VEEQEQE-AKHERIENDVATLSRRIAVEYSDS 546  
; RESULT 9  
US-10-467-657-2638  
; Sequence 2638, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRION SPA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASTIGNANI Vega  
; APPLICANT: MONACI Eliabatia  
; APPLICANT: MONACI Eliabatia  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIORITY APPLICATION NUMBER: GB-0103424.8  
; PRIORITY FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 2638  
; LENGTH: 244  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
; US-10-467-2638  
; Query Match 2.8%; Score 211; DB 6; Length 244;  
; Best Local Similarity 28.3%; Pred. No. 1e-06;  
; Matches 68; Conservative 41; Mismatches 117; Indels 14; Gaps 6;  
; APPLICANT: Cytokinetics, Inc.



PRIOR APPLICATION NUMBER: US 60/573,600  
 PRIORITY FILING DATE: 2004-05-20  
 NUMBER OF SEQ ID NOS: 26  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 8  
 LENGTH: 501  
 TYPE: PRT  
 ORGANISM: *Rattus norvegicus*  
 US-11-134-563-8

Query Match 2.6%; Score 194.5; DB 7; Length 501;  
 Best Local Similarity 32.4%; Pred. No. 2.8e-05;  
 Matches 60; Conservative 12; Mismatches 76; Indels 37; Gaps 7;  
 Qy 82 PPPMPMPSAQGRPPCPICPRPPFENHQMHRHPPVPPCFCPPMPPMPMCEN-NPPVGAQQGQ 139  
 Db 274 PPPPPSSRGGRPPP---PPPHSSGPPPPARGRGAPPFSRAFTAAPPPPSRPGV 329  
 Qy 140 GTPPFMPPPMPPNPHPPPPVWVQVQVYQPGYSHNFPFSPFNSFQNNSFLSANN 199  
 Db 330 VVPP--PPPNMYPPPNMPALSSAPSGPPP-----PPPL-----SMAGS 366  
 Qy 200 SSPPHERHLPPLPKAPSERRSERPERLKHDDHRHRSRDRRGASPDRR 259  
 Db 367 TAP----PPPPPPPGPPPPGLPSDGHQVASS--GNKAALDQIREGAKVKKV 418  
 Qy 260 RODSR 264  
 Db 419 EQNSR 423

RESULT 13  
 US-11-150-845-16  
 Sequence 16, Application US/11150845  
 Publication No. US20060003399A1  
 GENERAL INFORMATION:  
 APPLICANT: Cytokinetics, Inc.  
 APPLICANT: Tomasevic, Nenad  
 APPLICANT: Jia, Zhiheng  
 APPLICANT: Skowicz, Roman  
 APPLICANT: Pierce, Daniel  
 APPLICANT: Finer, Jeffrey  
 TITLE OF INVENTION: HIGH THROUGHPUT ACTIN POLYMERIZATION ASSAY  
 FILE REFERENCE: 020552-007720US  
 CURRENT APPLICATION NUMBER: US/11/150,845  
 CURRENT FILING DATE: 2005-06-10  
 PRIOR APPLICATION NUMBER: US 60/673,444  
 PRIOR FILING DATE: 2005-04-20  
 PRIOR APPLICATION NUMBER: 60/578,949  
 PRIOR FILING DATE: 2004-06-10  
 NUMBER OF SEQ ID NOS: 78  
 SOFTWARE: PatentIn version 3.3  
 SEQ ID NO: 14  
 LENGTH: 715  
 TYPE: PRT  
 ORGANISM: Artificial  
 OTHER INFORMATION: Myc-N-WASP-TAP fusion protein  
 US-11-150-845-16

Query Match 2.5%; Score 191; DB 7; Length 715;  
 Best Local Similarity 21.8%; Pred. No. 7.3e-05;  
 Matches 90; Conservative 41; Mismatches 130; Indels 152; Gaps 16;  
 Qy 80 PPPPPMP-----AQGPPCP--IRPPPNHOMRHPPVPPCFCPPM 120  
 Db 333 PLPPPPSSRGGNQLRPPIVGGNKGSGLPPVPLGAPPT--PRGPPPPGGGPP 390  
 Qy 39 LRLUHPPQOPPVQYQEPSPAPSITFSNPSAPFLPPRDPVFPVPPMPSAQQGPPCP 98  
 Db 294 LRLQAPPPPPSRGGPPPPPPHSSGPPPP--PARGRGAPPPPSRAPTAAPPPPPS 350  
 Qy 99 R-----PPFPNQMRHPPVPPCPFCPPMPPCPN---NPVPGAGPGCTFPFMP 148  
 Db 351 RISVEVPPPPRMYPPPPALSSAASGPPPPPSVILGVVAAPP-----PP 401  
 Qy 149 PMPMPHPPPPVWVQVNVYQVPPGQYSHNFPSPFNSFQNNSFLPSANNSSSPHRHLR 208

RESULT 14  
 US-11-150-845-14  
 Sequence 14, Application US/11150845  
 Publication No. US20060003399A1  
 GENERAL INFORMATION:  
 APPLICANT: Cytokinetics, Inc.  
 APPLICANT: Tomasevic, Nenad  
 APPLICANT: Jia, Zhiheng  
 APPLICANT: Skowicz, Roman  
 APPLICANT: Pierce, Daniel  
 APPLICANT: Finer, Jeffrey  
 TITLE OF INVENTION: HIGH THROUGHPUT ACTIN POLYMERIZATION ASSAY  
 FILE REFERENCE: 020552-007720US  
 CURRENT APPLICATION NUMBER: US/11/150,845  
 CURRENT FILING DATE: 2005-06-10  
 PRIOR APPLICATION NUMBER: US 60/673,444  
 PRIOR FILING DATE: 2005-04-20  
 PRIOR APPLICATION NUMBER: 60/578,949  
 PRIOR FILING DATE: 2004-06-10  
 NUMBER OF SEQ ID NOS: 78  
 SOFTWARE: PatentIn version 3.3  
 SEQ ID NO: 14  
 LENGTH: 715  
 TYPE: PRT  
 ORGANISM: Artificial  
 OTHER INFORMATION: Myc-WASP-TAP fusion protein  
 US-11-150-845-14

Query Match 2.5%; Score 191; DB 7; Length 715;  
 Best Local Similarity 21.8%; Pred. No. 7.3e-05;  
 Matches 90; Conservative 41; Mismatches 130; Indels 152; Gaps 16;  
 Qy 80 PPPPPMP-----AQGPPCP--IRPPPNHOMRHPPVPPCFCPPM 120  
 Db 333 PLPPPPSSRGGNQLRPPIVGGNKGSGLPPVPLGAPPT--PRGPPPPGGGPP 390  
 Qy 121 PPPMPCPNPPVPGAPPGQGTFPPMPPRSPHPPPPMPPQVQVYQVPPGQYSHNFP 180  
 Db 391 PPPATGRGSGLPPPPGAG-----GPPMPPPP-----PP 424  
 Qy 181 SFNSFQNNSFLSANNSSSPHRHLRPPKAPSERRSERPERLKHDDHRHRSRDR 240  
 Db 425 -----PSSGNGPAP-----PLPLPALVPGGLAP-----G 449  
 Qy 241 GRRHSLDRRERG---RSPD-----RRDQSRYSYDR 271  
 Db 450 GGRGALDQIROGQIQLNKTCGAPESALQPPQSSBGLVGAQMLHMWQKRSRAHSDEGE 509

RESULT 15  
 US-11-150-845-12  
 ; Sequence 12, Application US/11150845  
 ; Publication No. US20060003399A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cytokinetics, Inc.  
 ; APPLICANT: Tomasevic, Nenad  
 ; APPLICANT: Jia, Zhihang  
 ; APPLICANT: Sakowicz, Roman  
 ; APPLICANT: Pierce, Daniel  
 ; APPLICANT: Finer, Jeffrey  
 ; TITLE OF INVENTION: HIGH THROUGHPUT ACTIN POLYMERIZATION ASSAY  
 ; FILE REFERENCE: 020552-007720US  
 ; CURRENT APPLICATION NUMBER: US/11/150,845  
 ; CURRENT FILING DATE: 2005-06-10  
 ; PRIOR APPLICATION NUMBER: US 60/673,444  
 ; PRIOR FILING DATE: 2005-04-20  
 ; PRIOR APPLICATION NUMBER: 60/578,949  
 ; PRIOR FILING DATE: 2004-06-10  
 ; NUMBER OF SEQ ID NOS: 78  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 12  
 ; LENGTH: 408  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-1150-845-12

Query Match 2,5%; Score 190.5; DB 7; Length 408;  
 Best Local Similarity 34.4%; Pred. No. 3.9e-05;  
 Matches 52; Conservative 9; Mismatches 59; Indels 31; Gaps 7;

Qy 19 PRGRGGHARGAPSFRPQNLRLHROQPPVQYQEPSPASPTTFSNSPAPNPLPPRPDF 78  
 Db 184 PSSRGG---PPPPPPPHN---SGPPPPPARGRGAPPSSRAPTAAPPP--PPSRPS 234  
 Qy 79 VFPFPMPMPSAQGLPQCPTRPPFPNQMRIFPFVPPFCPPNPPMPCPMPVPCAPP 138  
 Db 235 VAVPPP-PPNRNPYPP--PALPSS-----APSGPPPPSVLGVGVPAPP-- 280  
 Qy 139 QGTFPFMPPPSMPPPPMPPQONYQY 169  
 Db 281 -----PppppGppppGlpSdgDhQvp 303

Search completed: February 3, 2006, 19:46:56  
 Job time : 17 sec

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